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<110> Barry,Caroline
       Bougueleret,Lydie
       Chumakov,Ilya
       Cohen-Akenine,Annick

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26

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28

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41

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42

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46

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47

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48

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49

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Ser Leu Ala Gln Gln Leu Gln Arg Leu Ala Leu Pro Gln Ser Asp Ala
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Ser Leu Leu Ser Arg Asp Glu Val Ala Ser Leu Leu Phe Asp Pro Lys
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gaa gcg gcc aca atc gac agg gac acc gcc ttc gcc att gga tgt act   262
Glu Ala Ala Thr Ile Asp Arg Asp Thr Ala Phe Ala Ile Gly Cys Thr
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Gly Leu Glu Glu Leu Leu Gly Ile Asp Pro Ser Phe Glu Gln Phe Glu
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Ala Pro Leu Phe Ser Gln Leu Ala Lys Thr Leu Glu Arg Ser Val Gln
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acc aaa gca gta aac aaa cag ttg gat gaa aac att tca tta ttc ctt   406
Thr Lys Ala Val Asn Lys Gln Leu Asp Glu Asn Ile Ser Leu Phe Leu
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Ile His Leu Ser Pro Tyr Phe Leu Leu Lys Pro Ala Gln Lys Cys Leu
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Glu Trp Leu Ile His Arg Phe His Ile His Leu Tyr Asn Gln Asp Ser
115   120   125   130

ctc att gct tgt gtt ctg cca tac cac gag aca aga ata ttt gtg cga   550
Leu Ile Ala Cys Val Leu Pro Tyr His Glu Thr Arg Ile Phe Val Arg
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Val Ile Gln Leu Leu Lys Ile Asn Asn Ser Lys His Arg Trp Phe Trp
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Leu Leu Pro Val Lys Gln Ser Gly Val Pro Leu Ala Lys Gly Thr Leu
         165   170   175

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Ile Thr His Cys Tyr Lys Asp Leu Gly Phe Met Asp Phe Ile Cys Ser
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Leu Val Thr Lys Ser Val Lys Val Phe Ala Glu Tyr Pro Gly Ser Ser
195   200   205   210

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Ala Gln Leu Arg Val Leu Leu Ala Phe Tyr Ala Ser Thr Ile Val Ser
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Ala Leu Val Ala Ala Glu Asp Val Ser Asp Asn Ile Ile Ala Lys Leu
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ttt ccc tat atc caa aag gga ttg aaa tca tct tta cca gat tac aga   886
Phe Pro Tyr Ile Gln Lys Gly Leu Lys Ser Ser Leu Pro Asp Tyr Arg
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gct gca aca tac atg ata ata tgt cag att tct gtg aaa gtg acc atg   934
Ala Ala Thr Tyr Met Ile Ile Cys Gln Ile Ser Val Lys Val Thr Met
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51

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acc aag att ccc tct ttg atc aag gat ggg tta agt tgc ttg ata gtg     1030
Thr Lys Ile Pro Ser Leu Ile Lys Asp Gly Leu Ser Cys Leu Ile Val
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Leu Leu Gln Arg Gln Lys Pro Glu Ser Leu Gly Lys Lys Pro Phe Pro
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cac tta tgt aat gtt cct gat ctt att aca ata ctt cat ggg att tct     1126
His Leu Cys Asn Val Pro Asp Leu Ile Thr Ile Leu His Gly Ile Ser
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gaa act tac gat gtc agt cct ctt ctg cgt tac atg ctt ccc cat ctg     1174
Glu Thr Tyr Asp Val Ser Pro Leu Leu Arg Tyr Met Leu Pro His Leu
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gtc gtc tcc atc att cat cat gtt aca gga gaa gaa act gaa gga atg     1222
Val Val Ser Ile Ile His His Val Thr Gly Glu Glu Thr Glu Gly Met
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gat ggt caa atc tac aag aga cac tta gaa gct ata ctt aca aaa ata     1270
Asp Gly Gln Ile Tyr Lys Arg His Leu Glu Ala Ile Leu Thr Lys Ile
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tca ctg aag aac aac tta gac cat ttg ttg gct agc ctt cta ttt gaa     1318
Ser Leu Lys Asn Asn Leu Asp His Leu Leu Ala Ser Leu Leu Phe Glu
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gag tat att tca tat agt tca cag gaa gaa atg gat tct aat aaa gtg     1366
Glu Tyr Ile Ser Tyr Ser Ser Gln Glu Glu Met Asp Ser Asn Lys Val
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Ser Leu Leu Asn Glu Gln Phe Leu Pro Leu Ile Arg Leu Leu Glu Ser
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aaa tac ccc aga aca tta gat gtt gta tta gag gaa cac tta aag gaa     1462
Lys Tyr Pro Arg Thr Leu Asp Val Val Leu Glu Glu His Leu Lys Glu
435                      440                      445                      450
att gca gat ctg aaa aaa caa gag ctt ttc cat cag ttt gtt tct ctt     1510
Ile Ala Asp Leu Lys Lys Gln Glu Leu Phe His Gln Phe Val Ser Leu
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Ser Thr Ser Gly Gly Lys Tyr Gln Phe Leu Ala Asp Ser Asp Thr Ser
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Leu Met Leu Ser Leu Asn His Pro Leu Ala Pro Val Arg Ile Leu Ala
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Met Asn His Leu Lys Lys Ile Met Lys Thr Ser Lys Glu Gly Val Asp
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His Phe Ser Ser Glu Val Thr Ile Ser Asn Leu Leu Asn Leu Phe Gln
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aga gca gaa ctt tca aag aat gga gaa tgg tac gag gta ctt aag ata     1846
Arg Ala Glu Leu Ser Lys Asn Gly Glu Trp Tyr Glu Val Leu Lys Ile
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gcc gct gac ata tta att aaa gaa gag ata ctg agt gaa aat gat cag     1894
Ala Ala Asp Ile Leu Ile Lys Glu Glu Ile Leu Ser Glu Asn Asp Gln
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52

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Lys Ser Gly Ile Cys Ser Leu His Pro Leu Leu Arg Gly Trp Glu Glu
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Gly Asp Pro Ser Ser Met Leu Lys Met Val Glu Asp Leu Ile Ser Val
675                 680                 685                 690
ggt gag gag gag tcc ttt aac ctg aag cag aaa gta acg ttt cat gtg    2230
Gly Glu Glu Glu Ser Phe Asn Leu Lys Gln Lys Val Thr Phe His Val
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Ile Leu Ser Val Leu Val Ser Cys Cys Ser Ser Leu Lys Glu Thr His
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Phe Pro Phe Ala Ile Arg Val Phe Ser Leu Leu Gln Lys Lys Ile Lys
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aag ctt gaa agt gtc att act gca gtg gaa atc ccc tca gaa tgg cac    2374
Lys Leu Glu Ser Val Ile Thr Ala Val Glu Ile Pro Ser Glu Trp His
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Tyr Val Glu Glu Leu Asn Ser Thr Gln Arg Val Ala Val Glu Asp Ser
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Val Phe Leu Val Phe Ser Leu Lys Lys Phe Ile Tyr Ala Leu Lys Ala
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cct aaa tct ttt cct aaa ggt gat ata tgg tgg aat cct gaa caa ctg    2566
Pro Lys Ser Phe Pro Lys Gly Asp Ile Trp Trp Asn Pro Glu Gln Leu
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aaa gaa gac agc agg gac tat ctg cac ttg ctc att ggg ctg ttt gag    2614
Lys Glu Asp Ser Arg Asp Tyr Leu His Leu Leu Ile Gly Leu Phe Glu
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Met Met Leu Asn Gly Ala Asp Ala Val His Phe Arg Val Leu Met Lys
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gca atg ctt tct tct cag aag aca cag tgt aaa cac caa ctg gca tcc    2854
Ala Met Leu Ser Ser Gln Lys Thr Gln Cys Lys His Gln Leu Ala Ser
        900                 905                 910
ata tct tct cca gtg gtg aca tct tta ctc att aac ctg gga agc ccc    2902
Ile Ser Ser Pro Val Val Thr Ser Leu Leu Ile Asn Leu Gly Ser Pro
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53

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gga gtg gca tcc ccg ttt tat ctg ata ata gat cat ttg att tct aaa        2998
Gly Val Ala Ser Pro Phe Tyr Leu Ile Ile Asp His Leu Ile Ser Lys
                950                 955                 960

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Ala Glu Glu Ile Thr Ser Asp Ala Ala Tyr Val Ile Gln Asp Leu Ala
                965                 970                 975

act tta ttt gag gaa cta cag aga gaa aag aaa ctg aaa tct cat cag        3094
Thr Leu Phe Glu Glu Leu Gln Arg Glu Lys Lys Leu Lys Ser His Gln
                980                 985                 990

aag ttg tct gaa act ttg aaa aac tta ctt agt tgt gtg tat agt tgc        3142
Lys Leu Ser Glu Thr Leu Lys Asn Leu Leu Ser Cys Val Tyr Ser Cys
995                 1000                1005                1010

cca tct tat ata gca aaa gat ttg atg aaa gta ctt cag gga gtc aac        3190
Pro Ser Tyr Ile Ala Lys Asp Leu Met Lys Val Leu Gln Gly Val Asn
                1015                1020                1025

ggt gag atg gtg ctt tct cag cta ttg cct atg gct gaa caa ctg cta        3238
Gly Glu Met Val Leu Ser Gln Leu Leu Pro Met Ala Glu Gln Leu Leu
                1030                1035                1040

gaa aag atc cag aag gag ccc aca gct gtg ctg aaa gat gag gcc atg        3286
Glu Lys Ile Gln Lys Glu Pro Thr Ala Val Leu Lys Asp Glu Ala Met
                1045                1050                1055

gtt ctg cat ctc act ctg gga aag tat aat gaa ttt tca gtt tcc ctt        3334
Val Leu His Leu Thr Leu Gly Lys Tyr Asn Glu Phe Ser Val Ser Leu
                1060                1065                1070

tta aat gag gat ccg aag agt cta gat ata ttt ata aaa gct gtg cac        3382
Leu Asn Glu Asp Pro Lys Ser Leu Asp Ile Phe Ile Lys Ala Val His
1075                1080                1085                1090

aca aca aag gaa ctt tac gcg gga atg cca acc att cag atc aca gcc        3430
Thr Thr Lys Glu Leu Tyr Ala Gly Met Pro Thr Ile Gln Ile Thr Ala
                1095                1100                1105

ctt gaa aag att aca aaa cca ttt ttt gca gcc ata tca gat gaa aaa        3478
Leu Glu Lys Ile Thr Lys Pro Phe Phe Ala Ala Ile Ser Asp Glu Lys
                1110                1115                1120

gtt cag cag aag ctt tta aga atg ttg ttt gat tta ttg gtg aac tgt        3526
Val Gln Gln Lys Leu Leu Arg Met Leu Phe Asp Leu Leu Val Asn Cys
                1125                1130                1135

aaa aac tca cat tgt gct cag act gtc agc agt gtt ttt aaa ggg att        3574
Lys Asn Ser His Cys Ala Gln Thr Val Ser Ser Val Phe Lys Gly Ile
                1140                1145                1150

tcc gtt aat gct gaa caa gtc cga ata gaa ctg gag cca cca gat aaa        3622
Ser Val Asn Ala Glu Gln Val Arg Ile Glu Leu Glu Pro Pro Asp Lys
1155                1160                1165                1170

gct aaa ccc ttg ggc aca gtt cag caa aaa aga agg caa aaa atg cag        3670
Ala Lys Pro Leu Gly Thr Val Gln Gln Lys Arg Arg Gln Lys Met Gln
                1175                1180                1185

cag aaa aaa tca caa gat cta gaa tct gtt cag gaa gtt gga ggt tct        3718
Gln Lys Lys Ser Gln Asp Leu Glu Ser Val Gln Glu Val Gly Gly Ser
                1190                1195                1200

tac tgg caa aga gta act ctc atc ctg gaa tta ctg cag cac aaa aag        3766
Tyr Trp Gln Arg Val Thr Leu Ile Leu Glu Leu Leu Gln His Lys Lys
                1205                1210                1215

aag ctc aga agt cct cag ata ttg gtg cca act ctt ttt aac ttg cta        3814
Lys Leu Arg Ser Pro Gln Ile Leu Val Pro Thr Leu Phe Asn Leu Leu
                1220                1225                1230

tca aga tgt tta gaa ccc ttg cca caa gag cag gga aat atg gaa tac        3862
Ser Arg Cys Leu Glu Pro Leu Pro Gln Glu Gln Gly Asn Met Glu Tyr
1235                1240                1245                1250

acc aaa caa tta att ctt agt tgt ctg ctc aac atc tgc caa aaa cta        3910
Thr Lys Gln Leu Ile Leu Ser Cys Leu Leu Asn Ile Cys Gln Lys Leu
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tct cca gat ggt ggc aaa ata ccc aaa gat att tta gat gag gag aag     3958
Ser Pro Asp Gly Gly Lys Ile Pro Lys Asp Ile Leu Asp Glu Glu Lys
          1270                    1275                    1280
ttc aac gtg gag ttg ata gtt cag tgc atc cgc ctt tcg gag atg ccg     4006
Phe Asn Val Glu Leu Ile Val Gln Cys Ile Arg Leu Ser Glu Met Pro
          1285                    1290                    1295
cag acc cat cac cat gcc ctt tta ctt ttg ggc act gtt gct gga ata     4054
Gln Thr His His His Ala Leu Leu Leu Leu Gly Thr Val Ala Gly Ile
          1300                    1305                    1310
ttt ccg gat aaa gtt tta cac aat atc atg tct att ttt aca ttt atg     4102
Phe Pro Asp Lys Val Leu His Asn Ile Met Ser Ile Phe Thr Phe Met
1315                    1320                    1325                    1330
gga gcc aat gtc atg cgc cta gat gat act tac agt ttt caa gtt att     4150
Gly Ala Asn Val Met Arg Leu Asp Asp Thr Tyr Ser Phe Gln Val Ile
                    1335                    1340                    1345
aac aag aca gtg aaa atg gtt att ccc gca ctt att cag tct gat agt     4198
Asn Lys Thr Val Lys Met Val Ile Pro Ala Leu Ile Gln Ser Asp Ser
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gga gat tct ata gaa gtt tca aga aac gtt gaa gag att gtg gta aaa     4246
Gly Asp Ser Ile Glu Val Ser Arg Asn Val Glu Glu Ile Val Val Lys
          1365                    1370                    1375
atc att agt gta ttt gtg gat gcg ctg cca cac gtc ccg gag cac agg     4294
Ile Ile Ser Val Phe Val Asp Ala Leu Pro His Val Pro Glu His Arg
          1380                    1385                    1390
cgc ctg ccc atc ctt gtt caa ctt gtt gat aca ctg ggt gca gag aaa     4342
Arg Leu Pro Ile Leu Val Gln Leu Val Asp Thr Leu Gly Ala Glu Lys
1395                    1400                    1405                    1410
ttc ctc tgg att ctc ctc atc ttg ctt ttt gaa cag tat gtc aca aaa     4390
Phe Leu Trp Ile Leu Leu Ile Leu Leu Phe Glu Gln Tyr Val Thr Lys
                    1415                    1420                    1425
aca gtg ctg gcg gct gcc tat ggc gaa aag gat gct att tta gaa gca     4438
Thr Val Leu Ala Ala Ala Tyr Gly Glu Lys Asp Ala Ile Leu Glu Ala
          1430                    1435                    1440
gac act gaa ttt tgg ttt tca gtc tgt tgt gag ttt agt gtc cag cat     4486
Asp Thr Glu Phe Trp Phe Ser Val Cys Cys Glu Phe Ser Val Gln His
          1445                    1450                    1455
cag ata caa agc ttg atg aat atc ctc cag tac tta cta aag ctg cca     4534
Gln Ile Gln Ser Leu Met Asn Ile Leu Gln Tyr Leu Leu Lys Leu Pro
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gag gaa aaa gaa gaa acc att ccc aaa gca gtg tca ttt aat aag agt     4582
Glu Glu Lys Glu Glu Thr Ile Pro Lys Ala Val Ser Phe Asn Lys Ser
1475                    1480                    1485                    1490
gaa tca caa gaa gaa atg cta cag gtt ttt aat gta gag act cac act     4630
Glu Ser Gln Glu Glu Met Leu Gln Val Phe Asn Val Glu Thr His Thr
                    1495                    1500                    1505
agc aag caa ctg cgg cat ttt aaa ttt ttg tca gtg tcc ttc atg tct     4678
Ser Lys Gln Leu Arg His Phe Lys Phe Leu Ser Val Ser Phe Met Ser
                    1510                    1515                    1520
cag ctc ctg tct tcc aat aat ttt ctg aaa aag gta gtt gag agt ggt     4726
Gln Leu Leu Ser Ser Asn Asn Phe Leu Lys Lys Val Val Glu Ser Gly
          1525                    1530                    1535
ggt cct gag att tta aaa ggc ctt gaa gag agg ttg ctg gag acc gtt     4774
Gly Pro Glu Ile Leu Lys Gly Leu Glu Glu Arg Leu Leu Glu Thr Val
          1540                    1545                    1550
ctc ggc tat atc agt gca gtt gca cag tcc atg gaa agg aac gca gac     4822
Leu Gly Tyr Ile Ser Ala Val Ala Gln Ser Met Glu Arg Asn Ala Asp
1555                    1560                    1565                    1570
aaa ctc acc gtg aag ttc tgg cgc gcg ctc ctt agt aaa gct tac gac     4870
Lys Leu Thr Val Lys Phe Trp Arg Ala Leu Leu Ser Lys Ala Tyr Asp
                    1575                    1580                    1585
ctg tta gat aag gtc aat gcc ttg ctg ccc aca gag aca ttc att cct     4918
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Leu Leu Asp Lys Val Asn Ala Leu Leu Pro Thr Glu Thr Phe Ile Pro
        1590                1595                1600
gtg atc aga ggg ctg gtg ggc aat ccc ctg cca tct gtt cgc cgc aaa      4965
Val Ile Arg Gly Leu Val Gly Asn Pro Leu Pro Ser Val Arg Arg Lys
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gcg ctg gac ctt ttg aat aac aag ctg cag caa aat ata tcc tgg aag      5014
Ala Leu Asp Leu Leu Asn Asn Lys Leu Gln Gln Asn Ile Ser Trp Lys
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aag aca ata gtt acc cgt ttc cta aaa ctg gtt cca gac ctt ttg gcc      5062
Lys Thr Ile Val Thr Arg Phe Leu Lys Leu Val Pro Asp Leu Leu Ala
1635                1640                1645                1650
att gtg cag cgt aag aaa aag gaa ggg gaa gaa gaa caa gca atc aac      5110
Ile Val Gln Arg Lys Lys Lys Glu Gly Glu Glu Glu Gln Ala Ile Asn
                1655                1660                1665
aga cag aca gcg ttg tat acc tta aag ctt tta tgc aag aat ttt ggt      5158
Arg Gln Thr Ala Leu Tyr Thr Leu Lys Leu Leu Cys Lys Asn Phe Gly
                1670                1675                1680
gca gaa aat cca gat cct ttt gtc cca gtg ctg arc act qct qtq aaa      5206
Ala Glu Asn Pro Asp Pro Phe Val Pro Val Leu Xaa Thr Ala Val Lys
        1685                1690                1695
ctg att gct cca gag aga aag gag gag aag aat gtc ytg gga agc gcg      5254
Leu Ile Ala Pro Glu Arg Lys Glu Glu Lys Asn Val Leu Gly Ser Ala
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ctg ctg tgc ata gca gag gtg acc tcc acc ctg gag gcg ctg gcc atc      5302
Leu Leu Cys Ile Ala Glu Val Thr Ser Thr Leu Glu Ala Leu Ala Ile
1715                1720                1725                1730
ccc cag ctt ccc agc ctg atg cca tcg ttg ctg aca aca atg aag aac      5350
Pro Gln Leu Pro Ser Leu Met Pro Ser Leu Leu Thr Thr Met Lys Asn
                1735                1740                1745
acc agc gag ctg gtc tcc agc gag gtc tac ctg ctc agt gcc ttg gct      5398
Thr Ser Glu Leu Val Ser Ser Glu Val Tyr Leu Leu Ser Ala Leu Ala
                1750                1755                1760
gct ctg cag aag gtt gtg gag act ctc ccg cac ttc atc agc ccc tat      5446
Ala Leu Gln Lys Val Val Glu Thr Leu Pro His Phe Ile Ser Pro Tyr
        1765                1770                1775
ctg gaa ggc att ctc tcc cag gtg att cat ctg gag aaa atc act agt      5494
Leu Glu Gly Ile Leu Ser Gln Val Ile His Leu Glu Lys Ile Thr Ser
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gaa atg ggt tct gcg tca cag gct aat atc cgt ctc aca tct ctt aaa      5542
Glu Met Gly Ser Ala Ser Gln Ala Asn Ile Arg Leu Thr Ser Leu Lys
1795                1800                1805                1810
aag aca ctg gct acc aca ctt gca ccc cga gtc ctg ttg ccc gcc atc      5590
Lys Thr Leu Ala Thr Thr Leu Ala Pro Arg Val Leu Leu Pro Ala Ile
                1815                1820                1825
aaa aaa act tac aag cag att gag aag aac tgg aag aat cac atg ggt      5638
Lys Lys Thr Tyr Lys Gln Ile Glu Lys Asn Trp Lys Asn His Met Gly
                1830                1835                1840
ccg ttt atg agc atc ttg caa gag cat att ggg gyg atg aag aag gaa      5686
Pro Phe Met Ser Ile Leu Gln Glu His Ile Gly Xaa Met Lys Lys Glu
        1845                1850                1855
gag ctc acc tcc cat cag tct cag cta acc gcc ttt ttc ctg gar gcc      5734
Glu Leu Thr Ser His Gln Ser Gln Leu Thr Ala Phe Phe Leu Glu Ala
        1860                1865                1870
ctg gac ttc cga gcc cag cac tct gag aac gat ctg gag gaa gtt gga      5782
Leu Asp Phe Arg Ala Gln His Ser Glu Asn Asp Leu Glu Glu Val Gly
1875                1880                1885                1890
aaa acg gaa aat tgt atc att gac tgt cta gta gcc atg gtt gtc aaa      5830
Lys Thr Glu Asn Cys Ile Ile Asp Cys Leu Val Ala Met Val Val Lys
                1895                1900                1905
ctt tcc gag gtc aca ttc agg ccc ctg ttc ttc aag ctg ttt gat tgg      5878
Leu Ser Glu Val Thr Phe Arg Pro Leu Phe Phe Lys Leu Phe Asp Trp
        1910                1915                1920
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gct aaa aca gaa gat gcc cca aag gac agg ttg ttg aca ttt tac aac      5926
Ala Lys Thr Glu Asp Ala Pro Lys Asp Arg Leu Leu Thr Phe Tyr Asn
        1925                1930                1935

ttg gca gat tgc att gct gaa aag ctg aaa ggg ctt ttt act ctg ttt      5974
Leu Ala Asp Cys Ile Ala Glu Lys Leu Lys Gly Leu Phe Thr Leu Phe
        1940                1945                1950

gcc ggc cac tta gtg aag cct ttt gct gac acc ttg rac cag gtg aac      6022
Ala Gly His Leu Val Lys Pro Phe Ala Asp Thr Leu Xaa Gln Val Asn
1955                1960                1965                1970

atc tcc aaa aca gat gaa gca ttt ttt gac tct gaa aat gac cct gaa      6070
Ile Ser Lys Thr Asp Glu Ala Phe Phe Asp Ser Glu Asn Asp Pro Glu
                1975                1980                1985

aag tgc tgc ttg ctg ttg cag ttt att ttg aac tgt tta tac aaa atc      6118
Lys Cys Cys Leu Leu Leu Gln Phe Ile Leu Asn Cys Leu Tyr Lys Ile
            1990                1995                2000

ttc ctt ttt gat acc cag cat ttt ata agt aaa gag aga gca gra gcc      6166
Phe Leu Phe Asp Thr Gln His Phe Ile Ser Lys Glu Arg Ala Xaa Ala
        2005                2010                2015

ttg atg atg cct ctg gtg gat cag ctg gaa aac agg ctt ggg gga gaa      6214
Leu Met Met Pro Leu Val Asp Gln Leu Glu Asn Arg Leu Gly Gly Glu
        2020                2025                2030

gag aaa ttc cag gaa cgg gtg aca aag cac ctg ata cca tgc atc gca      6262
Glu Lys Phe Gln Glu Arg Val Thr Lys His Leu Ile Pro Cys Ile Ala
2035                2040                2045                2050

cag ttt tcr gtg gcc atg gcg gat gac tct ctt tgg aaa cca ctg aac      6310
Gln Phe Ser Val Ala Met Ala Asp Asp Ser Leu Trp Lys Pro Leu Asn
                2055                2060                2065

tac cag att ctg cta aag acg aga gac tcc tcg cct aag gtt cga ttt      6358
Tyr Gln Ile Leu Leu Lys Thr Arg Asp Ser Ser Pro Lys Val Arg Phe
            2070                2075                2080

gct gct ttg att act gtg tta gca ctg gct gaa aaa cta aag gag aat      6406
Ala Ala Leu Ile Thr Val Leu Ala Leu Ala Glu Lys Leu Lys Glu Asn
        2085                2090                2095

tat att gtc ttg cta cca gaa tcc att cct ttc tta gca gag ttg atg      6454
Tyr Ile Val Leu Leu Pro Glu Ser Ile Pro Phe Leu Ala Glu Leu Met
        2100                2105                2110

gaa gat gaa tgt gaa gaa gta gaa cat cag tgc caa aag act att cag      6502
Glu Asp Glu Cys Glu Glu Val Glu His Gln Cys Gln Lys Thr Ile Gln
2115                2120                2125                2130

caa ctg gaa act gtc ctg gga gag cca ctc cag agc tat ttc taa         6547
Gln Leu Glu Thr Val Leu Gly Glu Pro Leu Gln Ser Tyr Phe  *
                2135                2140                2145
gactttctgt ggtgtttcat actctactca gagttcacac tcatatttca tattttatt    6607
tttgggtgtt gggtgccatg ttacttttgg tgccttaata cacctacttg gattacttac    6667
aaatgtttta tcacttcgtt acaaaatccc cacctggctt gtgctgccac ataagcctct    6727
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                                                          Met Thr
                                                           1
tcc tta gcc cag cag ctg caa cga ctc gcc ctc cct caa agt gat gcc   166
Ser Leu Ala Gln Gln Leu Gln Arg Leu Ala Leu Pro Gln Ser Asp Ala
         5   10   15
agc ctc tta tcy aga gat gaa gtt gct tct ttg tta ttt gac cct aag   214
Ser Leu Leu Ser Arg Asp Glu Val Ala Ser Leu Leu Phe Asp Pro Lys

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         20                      25                      30
gaa gcg gcc aca atc gac agg gac acc gcc ttc gcc att gga tgt act    262
Glu Ala Ala Thr Ile Asp Arg Asp Thr Ala Phe Ala Ile Gly Cys Thr
35                  40                  45                  50
ggc ctg gaa gag ttg ctt gga att gat cct tcc ttt gag cag ttt gaa    310
Gly Leu Glu Glu Leu Leu Gly Ile Asp Pro Ser Phe Glu Gln Phe Glu
                55                  60                  65
gca ccg ttg ttc agt cag cta gca aaa acc ttg gag cga agt gtt cag    358
Ala Pro Leu Phe Ser Gln Leu Ala Lys Thr Leu Glu Arg Ser Val Gln
            70                  75                  80
acc aaa gca gta aac aaa cag ttg gat gaa aac att tca tta ttc ctt    406
Thr Lys Ala Val Asn Lys Gln Leu Asp Glu Asn Ile Ser Leu Phe Leu
        85                  90                  95
att cac ttg tcg cct tac ttc ctg ctt aag cca gca cag aag tgt ctg    454
Ile His Leu Ser Pro Tyr Phe Leu Leu Lys Pro Ala Gln Lys Cys Leu
    100                 105                 110
gag tgg ttg att cac agg ttc cat ata cat ctc tat aat caa gat agc    502
Glu Trp Leu Ile His Arg Phe His Ile His Leu Tyr Asn Gln Asp Ser
115                 120                 125                 130
ctc att gct tgt gtt ctg cca tac cac gag aca aga ata ttt gtg cga    550
Leu Ile Ala Cys Val Leu Pro Tyr His Glu Thr Arg Ile Phe Val Arg
                135                 140                 145
gtc ata cag ctt cta aaa att aat aat tca aag cac aga tgg ttc tgg    598
Val Ile Gln Leu Leu Lys Ile Asn Asn Ser Lys His Arg Trp Phe Trp
            150                 155                 160
ttg ttg cca gtt aag caa tct gga gtg ccg tta gct aaa gga act ttg    646
Leu Leu Pro Val Lys Gln Ser Gly Val Pro Leu Ala Lys Gly Thr Leu
        165                 170                 175
att acc cac tgc tac aaa gat ctt gga ttc atg gat ttc att tgc agt    694
Ile Thr His Cys Tyr Lys Asp Leu Gly Phe Met Asp Phe Ile Cys Ser
    180                 185                 190
ttg gtg aca aaa tct gtg aag gtt ttt gct gag tac ccg ggc agc tca    742
Leu Val Thr Lys Ser Val Lys Val Phe Ala Glu Tyr Pro Gly Ser Ser
195                 200                 205                 210
gct cag ttg agg gtg ctc ttg gct ttc tat gct tct acc ata gtg tcg    790
Ala Gln Leu Arg Val Leu Leu Ala Phe Tyr Ala Ser Thr Ile Val Ser
                215                 220                 225
gcg ctg gta gct gca gag gac gta tca gac aat atc atc gcc aaa cta    838
Ala Leu Val Ala Ala Glu Asp Val Ser Asp Asn Ile Ile Ala Lys Leu
            230                 235                 240
ttt ccc tat atc caa aag gga ttg aaa tca tct tta cca gat tac aga    886
Phe Pro Tyr Ile Gln Lys Gly Leu Lys Ser Ser Leu Pro Asp Tyr Arg
        245                 250                 255
gct gca aca tac atg ata ata tgt cag att tct gtg aaa gtg acc atg    934
Ala Ala Thr Tyr Met Ile Ile Cys Gln Ile Ser Val Lys Val Thr Met
    260                 265                 270
gaa aat acc ttt gtg aat tca ttg gca tca cag atc atc aaa aca ttg    982
Glu Asn Thr Phe Val Asn Ser Leu Ala Ser Gln Ile Ile Lys Thr Leu
275                 280                 285                 290
acc aag att ccc tct ttg atc aag gat ggg tta agt tgc ttg ata gtg    1030
Thr Lys Ile Pro Ser Leu Ile Lys Asp Gly Leu Ser Cys Leu Ile Val
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ctc ctg cag aga cag aag cca gag agc ctt ggg aaa aag cca ttc cct    1078
Leu Leu Gln Arg Gln Lys Pro Glu Ser Leu Gly Lys Lys Pro Phe Pro
                310                 315                 320
cac tta tgt aat gtt cct gat ctt att aca ata ctt cat ggg att tct    1126
His Leu Cys Asn Val Pro Asp Leu Ile Thr Ile Leu His Gly Ile Ser
            325                 330                 335
gaa act tac gat gtc agt cct ctt ctg cgt tac atg ctt ccc cat ctg    1174
Glu Thr Tyr Asp Val Ser Pro Leu Leu Arg Tyr Met Leu Pro His Leu
        340                 345                 350
gtc gtc tcc atc att cat cat gtt aca gga gaa gaa act gaa gga atg    1222
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Val Val Ser Ile Ile His His Val Thr Gly Glu Glu Thr Glu Gly Met
355                 360             365             370
gat ggt caa atc tac aag aga cac tta gaa gct ata ctt aca aaa ata    1270
Asp Gly Gln Ile Tyr Lys Arg His Leu Glu Ala Ile Leu Thr Lys Ile
                375             380             385
tca ctg aag aac aac tta gac cat ttg ttg gct agc ctt cta ttt gaa    1318
Ser Leu Lys Asn Asn Leu Asp His Leu Leu Ala Ser Leu Leu Phe Glu
                390             395             400
gag tat att tca tat agt tca cag gaa gaa atg gat tct aat aaa gtg    1366
Glu Tyr Ile Ser Tyr Ser Ser Gln Glu Glu Met Asp Ser Asn Lys Val
            405             410             415
tct ttg ctt aat gaa caa ttt ctt cca ctc att aga ctt tta gaa agc    1414
Ser Leu Leu Asn Glu Gln Phe Leu Pro Leu Ile Arg Leu Leu Glu Ser
        420             425             430
aaa tac ccc aga aca tta gat gtt gta tta gag gaa cac tta aag gaa    1462
Lys Tyr Pro Arg Thr Leu Asp Val Val Leu Glu Glu His Leu Lys Glu
435             440             445             450
att gca gat ctg aaa aaa caa gag ctt ttc cat cag ttt gtt tct ctt    1510
Ile Ala Asp Leu Lys Lys Gln Glu Leu Phe His Gln Phe Val Ser Leu
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tct aca agt gga gga aag tat cag ttt tta gca gat tct gat act tct    1558
Ser Thr Ser Gly Gly Lys Tyr Gln Phe Leu Ala Asp Ser Asp Thr Ser
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Leu Met Leu Ser Leu Asn His Pro Leu Ala Pro Val Arg Ile Leu Ala
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Met Asn His Leu Lys Lys Ile Met Lys Thr Ser Lys Glu Gly Val Asp
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Glu Ser Phe Ile Lys Glu Ala Val Leu Ala Arg Leu Gly Asp Asp Asn
515             520             525             530
ata gat gtt gtt ttg tcg gct ata agt gct ttt gag att ttc aaa gaa    1750
Ile Asp Val Val Leu Ser Ala Ile Ser Ala Phe Glu Ile Phe Lys Glu
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His Phe Ser Ser Glu Val Thr Ile Ser Asn Leu Leu Asn Leu Phe Gln
            550             555             560
aga gca gaa ctt tca aag aat gga gaa tgg tac gag gta ctt aag ata    1846
Arg Ala Glu Leu Ser Lys Asn Gly Glu Trp Tyr Glu Val Leu Lys Ile
            565             570             575
gcc gct gac ata tta att aaa gaa gag ata ctg agt gaa aat gat cag    1894
Ala Ala Asp Ile Leu Ile Lys Glu Glu Ile Leu Ser Glu Asn Asp Gln
            580             585             590
ttg tca aat cag gtg gtt gta tgt ttg ctg cca ttt gtg gtt atc aat    1942
Leu Ser Asn Gln Val Val Val Cys Leu Leu Pro Phe Val Val Ile Asn
595             600             605             610
aat gat gat acg gaa tct gct gag atg aaa att gct ata tat tta tca    1990
Asn Asp Asp Thr Glu Ser Ala Glu Met Lys Ile Ala Ile Tyr Leu Ser
            615             620             625
aaa tca gga atc tgc tcc ctg cac cct cta tta aga ggc tgg gaa gaa    2038
Lys Ser Gly Ile Cys Ser Leu His Pro Leu Leu Arg Gly Trp Glu Glu
            630             635             640
gct ctt gaa aat gta att aaa agc aca aag cca gga aaa cta atc ggt    2086
Ala Leu Glu Asn Val Ile Lys Ser Thr Lys Pro Gly Lys Leu Ile Gly
            645             650             655
gta gca aat cag aag atg att gag ttg ttg gct gat aat ata aat tta    2134
Val Ala Asn Gln Lys Met Ile Glu Leu Leu Ala Asp Asn Ile Asn Leu
            650             665             670
gga gat cct tct tca atg tta aag atg gtg gag gat ttg ata agc gtg    2182
Gly Asp Pro Ser Ser Met Leu Lys Met Val Glu Asp Leu Ile Ser Val
675             680             685             690
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60

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ggt gag gag gag tcc ttt aac ctg aag cag aaa gta acg ttt cat gtg        2230
Gly Glu Glu Glu Ser Phe Asn Leu Lys Gln Lys Val Thr Phe His Val
            695                     700                 705

atc ctg tct gtg ctc gtc tct tgt tgt tca tct tta aaa gaa acc cac        2278
Ile Leu Ser Val Leu Val Ser Cys Cys Ser Ser Leu Lys Glu Thr His
            710                 715                 720

ttt cca ttt gcg ata aga gtc ttc agt ttg ttg cag aaa aaa ata aag        2326
Phe Pro Phe Ala Ile Arg Val Phe Ser Leu Leu Gln Lys Lys Ile Lys
            725                 730                 735

aag ctt gaa agt gtc att act gca gtg gaa atc ccc tca gaa tgg cac        2374
Lys Leu Glu Ser Val Ile Thr Ala Val Glu Ile Pro Ser Glu Trp His
            740                 745                 750

att gaa ctg atg tta gac aga ggg atc cca gta gag ctg tgg gca cat        2422
Ile Glu Leu Met Leu Asp Arg Gly Ile Pro Val Glu Leu Trp Ala His
755                     760                 765                 770

tat gta gaa gag ctc aac agc act cag agg gtg gcc gtg gag gac tcg        2470
Tyr Val Glu Glu Leu Asn Ser Thr Gln Arg Val Ala Val Glu Asp Ser
                775                 780                 785

gtt ttt ctt gta ttt tcc ttg aaa aaa ttt att tat gca ctg aaa gct        2518
Val Phe Leu Val Phe Ser Leu Lys Lys Phe Ile Tyr Ala Leu Lys Ala
            790                 795                 800

cct aaa tct ttt cct aaa ggt gat ata tgg tgg aat cct gaa caa ctg        2566
Pro Lys Ser Phe Pro Lys Gly Asp Ile Trp Trp Asn Pro Glu Gln Leu
            805                 810                 815

aaa gaa gac agc agg gac tat ctg cac ttg ctc att ggg ctg ttt gag        2614
Lys Glu Asp Ser Arg Asp Tyr Leu His Leu Leu Ile Gly Leu Phe Glu
            820                 825                 830

atg atg ctc aat ggt gcc gat gct gtt cat ttc aga gtt ctg atg aaa        2662
Met Met Leu Asn Gly Ala Asp Ala Val His Phe Arg Val Leu Met Lys
835                     840                 845                 850

ctt ttc ata aag gtk cat cta gaa gat gtt ttt cag tta ttc aag ttc        2710
Leu Phe Ile Lys Val His Leu Glu Asp Val Phe Gln Leu Phe Lys Phe
            855                 860                 865

tgt tct gtt tta tgg acc tat ggt tct agc ctt tca aat cca cta aac        2758
Cys Ser Val Leu Trp Thr Tyr Gly Ser Ser Leu Ser Asn Pro Leu Asn
            870                 875                 880

tgc agt gtg aaa aca gtg ctg cag act caa gct ctt tat gtg ggc tgt        2806
Cys Ser Val Lys Thr Val Leu Gln Thr Gln Ala Leu Tyr Val Gly Cys
            885                 890                 895

gca atg ctt tct tct cag aag aca cag tgt aaa cac caa ctg gca tcc        2854
Ala Met Leu Ser Ser Gln Lys Thr Gln Cys Lys His Gln Leu Ala Ser
            900                 905                 910

ata tct tct cca gtg gtg aca tct tta ctc att aac ctg gga agc ccc        2902
Ile Ser Ser Pro Val Val Thr Ser Leu Leu Ile Asn Leu Gly Ser Pro
915                     920                 925                 930

gta aaa gaa gtt cgt agg gct gcc att cag tgt ctc cag gcc ctc agt        2950
Val Lys Glu Val Arg Arg Ala Ala Ile Gln Cys Leu Gln Ala Leu Ser
                935                 940                 945

gga gtg gca tcc ccg ttt tat ctg ata ata gat cat ttg att tct aaa        2998
Gly Val Ala Ser Pro Phe Tyr Leu Ile Ile Asp His Leu Ile Ser Lys
                950                 955                 960

gca gag gag atc act tca gat gct gcc tat gtt att cag gat ttg gct        3046
Ala Glu Glu Ile Thr Ser Asp Ala Ala Tyr Val Ile Gln Asp Leu Ala
            965                 970                 975

act tta ttt gag gaa cta cag aga gaa aag aaa ctg aaa tct cat cag        3094
Thr Leu Phe Glu Glu Leu Gln Arg Glu Lys Lys Leu Lys Ser His Gln
            980                 985                 990

aag ttg tct gaa act ttg aaa aac tta ctt agt tgt gtg tat agt tgc        3142
Lys Leu Ser Glu Thr Leu Lys Asn Leu Leu Ser Cys Val Tyr Ser Cys
995                     1000                1005                1010

cca tct tat ata gca aaa gat ttg atg aaa gta ctt cag gga gtc aac        3190
Pro Ser Tyr Ile Ala Lys Asp Leu Met Lys Val Leu Gln Gly Val Asn
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ggt gag atg gtg ctt tct cag cta ttg cct atg gct gaa caa ctg cta          3238
Gly Glu Met Val Leu Ser Gln Leu Leu Pro Met Ala Glu Gln Leu Leu
         1030                    1035                    1040
gaa aag atc cag aag gag ccc aca gct gtg ctg aaa gat gag gcc atg          3285
Glu Lys Ile Gln Lys Glu Pro Thr Ala Val Leu Lys Asp Glu Ala Met
              1045                    1050                    1055
gtt ctg cat ctc act ctg gga aag tat aat gaa ttt tca gtt tcc ctt          3334
Val Leu His Leu Thr Leu Gly Lys Tyr Asn Glu Phe Ser Val Ser Leu
    1060                    1065                    1070
tta aat gag gat ccg aag agt cta gat ata ttt ata aaa gct gtg cac          3382
Leu Asn Glu Asp Pro Lys Ser Leu Asp Ile Phe Ile Lys Ala Val His
1075                    1080                    1085                    1090
aca aca aag gaa ctt tac gcg gga atg cca acc att cag atc aca gcc          3430
Thr Thr Lys Glu Leu Tyr Ala Gly Met Pro Thr Ile Gln Ile Thr Ala
              1095                    1100                    1105
ctt gaa aag att aca aaa cca ttt ttt gca gcc ata tca gat gaa aaa          3478
Leu Glu Lys Ile Thr Lys Pro Phe Phe Ala Ala Ile Ser Asp Glu Lys
              1110                    1115                    1120
gtt cag cag aag ctt tta aga atg ttg ttt gat tta ttg gtg aac tgt          3526
Val Gln Gln Lys Leu Leu Arg Met Leu Phe Asp Leu Leu Val Asn Cys
         1125                    1130                    1135
aaa aac tca cat tgt gct cag act gtc agc agt gtt ttt aaa ggg att          3574
Lys Asn Ser His Cys Ala Gln Thr Val Ser Ser Val Phe Lys Gly Ile
         1140                    1145                    1150
tcc gtt aat gct gaa caa gtc cga ata gaa ctg gag cca cca gat aaa          3622
Ser Val Asn Ala Glu Gln Val Arg Ile Glu Leu Glu Pro Pro Asp Lys
1155                    1160                    1165                    1170
gct aaa ccc ttg ggc aca gtt cag caa aaa aga agg caa aaa atg cag          3670
Ala Lys Pro Leu Gly Thr Val Gln Gln Lys Arg Arg Gln Lys Met Gln
              1175                    1180                    1185
cag aaa aaa tca caa gat cta gaa tct gtt cag gaa gtt gga ggt tct          3718
Gln Lys Lys Ser Gln Asp Leu Glu Ser Val Gln Glu Val Gly Gly Ser
         1190                    1195                    1200
tac tgg caa aga gta act ctc atc ctg gaa tta ctg cag cac aaa aag          3766
Tyr Trp Gln Arg Val Thr Leu Ile Leu Glu Leu Leu Gln His Lys Lys
         1205                    1210                    1215
aag ctc aga agt cct cag ata ttg gtg cca act ctt ttt aac ttg cta          3814
Lys Leu Arg Ser Pro Gln Ile Leu Val Pro Thr Leu Phe Asn Leu Leu
         1220                    1225                    1230
tca aga tgt tta gaa ccc ttg cca caa gag cag gga aat atg gaa tac          3862
Ser Arg Cys Leu Glu Pro Leu Pro Gln Glu Gln Gly Asn Met Glu Tyr
1235                    1240                    1245                    1250
acc aaa caa tta att ctt agt tgt ctg ctc aac atc tgc caa aaa cta          3910
Thr Lys Gln Leu Ile Leu Ser Cys Leu Leu Asn Ile Cys Gln Lys Leu
              1255                    1260                    1265
tct cca gat ggt ggc aaa ata ccc aaa gat att tta gat gag gag aag          3958
Ser Pro Asp Gly Gly Lys Ile Pro Lys Asp Ile Leu Asp Glu Glu Lys
              1270                    1275                    1280
ttc aac gtg gag ttg ata gtt cag tgc atc cgc ctt tcg gag atg ccg          4006
Phe Asn Val Glu Leu Ile Val Gln Cys Ile Arg Leu Ser Glu Met Pro
              1285                    1290                    1295
cag acc cat cac cat gcc ctt tta ctt ttg ggc act gtt gct gga ata          4054
Gln Thr His His His Ala Leu Leu Leu Leu Gly Thr Val Ala Gly Ile
         1300                    1305                    1310
ttt ccg gat aaa gtt tta cac aat atc atg tct att ttt aca ttt atg          4102
Phe Pro Asp Lys Val Leu His Asn Ile Met Ser Ile Phe Thr Phe Met
1315                    1320                    1325                    1330
gga gcc aat gtc atg cgc cta gat gat act tac agt ttt caa gtt att          4150
Gly Ala Asn Val Met Arg Leu Asp Asp Thr Tyr Ser Phe Gln Val Ile
         1335                    1340                    1345
aac aag aca gtg aaa atg gtt att ccc gca ctt att cag tct gat agt          4198
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Asn Lys Thr Val Lys Met Val Ile Pro Ala Leu Ile Gln Ser Asp Ser
          1350                1355                1360
gga gat tct ata gaa gtt tca aga aac gtt gaa gag att gtg gta aaa    4246
Gly Asp Ser Ile Glu Val Ser Arg Asn Val Glu Glu Ile Val Val Lys
          1365                1370                1375
atc att agt gta ttt gtg gat gcg ctg cca cac gtc ccg gag cac agg    4294
Ile Ile Ser Val Phe Val Asp Ala Leu Pro His Val Pro Glu His Arg
          1380                1385                1390
cgc ctg ccc atc ctt gtt caa ctt gtt gat aca ctg ggt gca gag aaa    4342
Arg Leu Pro Ile Leu Val Gln Leu Val Asp Thr Leu Gly Ala Glu Lys
1395                1400                1405                1410
ttc ctc tgg att ctc ctc atc ttg ctt ttt gaa cag tat gtc aca aaa    4390
Phe Leu Trp Ile Leu Leu Ile Leu Leu Phe Glu Gln Tyr Val Thr Lys
                    1415                1420                1425
aca gtg ctg gcg gct gcc tat ggc gaa aag gat gct att tta gaa gca    4438
Thr Val Leu Ala Ala Ala Tyr Gly Glu Lys Asp Ala Ile Leu Glu Ala
              1430                1435                1440
gac act gaa ttt tgg ttt tca gtc tgt tgt gag ttt agt gtc cag cat    4486
Asp Thr Glu Phe Trp Phe Ser Val Cys Cys Glu Phe Ser Val Gln His
              1445                1450                1455
cag ata caa agc ttg atg aat atc ctc cag tac tta cta aag ctg cca    4534
Gln Ile Gln Ser Leu Met Asn Ile Leu Gln Tyr Leu Leu Lys Leu Pro
          1460                1465                1470
gag gaa aaa gaa gaa acc att ccc aaa gca gtg tca ttt aat aag agt    4582
Glu Glu Lys Glu Glu Thr Ile Pro Lys Ala Val Ser Phe Asn Lys Ser
1475                1480                1485                1490
gaa tca caa gaa gaa atg cta cag gtt ttt aat gta gag act cac act    4630
Glu Ser Gln Glu Glu Met Leu Gln Val Phe Asn Val Glu Thr His Thr
                    1495                1500                1505
agc aag caa ctg cgg cat ttt aaa ttt ttg tca gtg tcc ttc atg tct    4678
Ser Lys Gln Leu Arg His Phe Lys Phe Leu Ser Val Ser Phe Met Ser
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cag ctc ctg tct tcc aat aat ttt ctg aaa aag gta gtt gag agt ggt    4726
Gln Leu Leu Ser Ser Asn Asn Phe Leu Lys Lys Val Val Glu Ser Gly
              1525                1530                1535
ggt cct gag att tta aaa ggc ctt gaa gag agg ttg ctg gag acc gtt    4774
Gly Pro Glu Ile Leu Lys Gly Leu Glu Glu Arg Leu Leu Glu Thr Val
          1540                1545                1550
ctc ggc tat atc agt gca gtt gca cag tcc atg gaa agg aac gca gac    4822
Leu Gly Tyr Ile Ser Ala Val Ala Gln Ser Met Glu Arg Asn Ala Asp
1555                1560                1565                1570
aaa ctc acc gtg aag ttc tgg cgc gcg ctc ctt agt aaa gct tac gac    4870
Lys Leu Thr Val Lys Phe Trp Arg Ala Leu Leu Ser Lys Ala Tyr Asp
                    1575                1580                1585
ctg tta gat aag gtc aat gcc ttg ctg ccc aca gag aca ttc att cct    4918
Leu Leu Asp Lys Val Asn Ala Leu Leu Pro Thr Glu Thr Phe Ile Pro
                    1590                1595                1600
gtg atc aga ggg ctg gtg ggc aat ccc ctg cca tct gtt cgc cgc aaa    4966
Val Ile Arg Gly Leu Val Gly Asn Pro Leu Pro Ser Val Arg Arg Lys
          1605                1610                1615
gcg ctg gac ctt ttg aat aac aag ctg cag caa aat ata tcc tgg aag    5014
Ala Leu Asp Leu Leu Asn Asn Lys Leu Gln Gln Asn Ile Ser Trp Lys
          1620                1625                1630
aag aca ata gtt acc cgt ttc cta aaa ctg gtt cca gac ctt ttg gcc    5062
Lys Thr Ile Val Thr Arg Phe Leu Lys Leu Val Pro Asp Leu Leu Ala
1635                1640                1645                1650
att gtg cag cgt aag aaa aag gaa ggg gaa gaa gaa caa gca atc aac    5110
Ile Val Gln Arg Lys Lys Lys Glu Gly Glu Glu Glu Gln Ala Ile Asn
          1655                1660                1665
aga cag aca gcg ttg tat acc tta aag ctt tta tgc aag aat ttt ggt    5158
Arg Gln Thr Ala Leu Tyr Thr Leu Lys Leu Leu Cys Lys Asn Phe Gly
          1670                1675                1680
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gca gaa aat cca gat cct ttt gtc cca gtg ctg arc act gct gtg aaa    5206
Ala Glu Asn Pro Asp Pro Phe Val Pro Val Leu Xaa Thr Ala Val Lys
        1685            1690                1695

ctg att gct cca gag aga aag gag gag aag aat gtc ytg gga agc gcg    5254
Leu Ile Ala Pro Glu Arg Lys Glu Glu Lys Asn Val Leu Gly Ser Ala
        1700            1705                1710

ctg ctg tgc ata gca gag gtg acc tcc acc ctg gag gcg ctg gcc atc    5302
Leu Leu Cys Ile Ala Glu Val Thr Ser Thr Leu Glu Ala Leu Ala Ile
1715            1720                1725                1730

ccc cag ctt ccc agc ctg atg cca tcg ttg ctg aca aca atg aag aac    5350
Pro Gln Leu Pro Ser Leu Met Pro Ser Leu Leu Thr Thr Met Lys Asn
                1735                1740                1745

acc agc gag ctg gtc tcc agc gag gtc tac ctg ctc agt gcc ttg gct    5398
Thr Ser Glu Leu Val Ser Ser Glu Val Tyr Leu Leu Ser Ala Leu Ala
                1750                1755                1760

gct ctg cag aag gtt gtg gag act ctc ccg cac ttc atc agc ccc tat    5446
Ala Leu Gln Lys Val Val Glu Thr Leu Pro His Phe Ile Ser Pro Tyr
        1765                1770                1775

ctg gaa ggc att ctc tcc cag gtg att cat ctg gag aaa atc act agt    5494
Leu Glu Gly Ile Leu Ser Gln Val Ile His Leu Glu Lys Ile Thr Ser
        1780                1785                1790

gaa atg ggt tct gcg tca cag gct aat atc cgt ctc aca tct ctt aaa    5542
Glu Met Gly Ser Ala Ser Gln Ala Asn Ile Arg Leu Thr Ser Leu Lys
1795                1800                1805                1810

aag aca ctg gct acc aca ctt gca ccc cga gtc ctg ttg ccc gcc atc    5590
Lys Thr Leu Ala Thr Thr Leu Ala Pro Arg Val Leu Leu Pro Ala Ile
                1815                1820                1825

aaa aaa act tac aag cag att gag aag aac tgg aag aat cac atg ggt    5638
Lys Lys Thr Tyr Lys Gln Ile Glu Lys Asn Trp Lys Asn His Met Gly
        1830                1835                1840

ccg ttt atg agc atc ttg caa gag cat att ggg gyg atg aag aag gaa    5686
Pro Phe Met Ser Ile Leu Gln Glu His Ile Gly Xaa Met Lys Lys Glu
        1845                1850                1855

gag ctc acc tcc cat cag tct cag cta acc gcc ttt ttc ctg gar gcc    5734
Glu Leu Thr Ser His Gln Ser Gln Leu Thr Ala Phe Phe Leu Glu Ala
        1860                1865                1870

ctg gac ttc cga gcc cag cac tct gag aac gat ctg gag gaa gtt gga    5782
Leu Asp Phe Arg Ala Gln His Ser Glu Asn Asp Leu Glu Glu Val Gly
1875                1880                1885                1890

aaa acg gaa aat tgt atc att gac tgt cta gta gcc atg gtt gtc aaa    5830
Lys Thr Glu Asn Cys Ile Ile Asp Cys Leu Val Ala Met Val Val Lys
                1895                1900                1905

ctt tcc gag gtc aca ttc agg ccc ctg ttc ttc aag ctg ttt gat tgg    5878
Leu Ser Glu Val Thr Phe Arg Pro Leu Phe Phe Lys Leu Phe Asp Trp
                1910                1915                1920

gct aaa aca gaa gat gcc cca aag gac agg ttg ttg aca ttt tac aac    5926
Ala Lys Thr Glu Asp Ala Pro Lys Asp Arg Leu Leu Thr Phe Tyr Asn
        1925                1930                1935

ttg gca gat tgc att gct gaa aag ctg aaa ggg ctt ttt act ctg ttt    5974
Leu Ala Asp Cys Ile Ala Glu Lys Leu Lys Gly Leu Phe Thr Leu Phe
        1940                1945                1950

gcc ggc cac tta gtg aag cct ttt gct gac acc ttg rac cag gtg aac    6022
Ala Gly His Leu Val Lys Pro Phe Ala Asp Thr Leu Xaa Gln Val Asn
1955            1960                1965                1970

atc tcc aaa aca gat gaa gca ttt ttt gac tct gaa aat gac cct gaa    6070
Ile Ser Lys Thr Asp Glu Ala Phe Phe Asp Ser Glu Asn Asp Pro Glu
                1975                1980                1985

aag tgc tgc ttg ctg ttg cag ttt att ttg aac tgt tta tac aaa atc    6118
Lys Cys Cys Leu Leu Leu Gln Phe Ile Leu Asn Cys Leu Tyr Lys Ile
                1990                1995                2000

ttc ctt ttt gat acc cag cat ttt ata agt aaa gag aga gca gra gcc    6166
Phe Leu Phe Asp Thr Gln His Phe Ile Ser Lys Glu Arg Ala Xaa Ala
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Leu Met Met Pro Leu Val Asp Gln Leu Glu Asn Arg Leu Gly Gly Glu
        2020                    2025                    2030
gag aaa ttc cag gaa cgg gtg aca aag cac ctg ata cca tgc atc gca      6252
Glu Lys Phe Gln Glu Arg Val Thr Lys His Leu Ile Pro Cys Ile Ala
2035                    2040                    2045                    2050
cag ttt tcr gtg gcc atg gcg gat gac tct ctt tgg aaa cca ctg aac      6310
Gln Phe Ser Val Ala Met Ala Asp Asp Ser Leu Trp Lys Pro Leu Asn
                        2055                    2060                    2065
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Tyr Gln Ile Leu Leu Lys Thr Arg Asp Ser Ser Pro Lys Val Arg Phe
                2070                    2075                    2080
gct gct ttg att act gtg tta gca ctg gct gaa aaa cta aag gag aat      6406
Ala Ala Leu Ile Thr Val Leu Ala Leu Ala Glu Lys Leu Lys Glu Asn
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tat att gtc ttg cta cca gaa tcc att cct ttc tta gca gag ttg atg      6454
Tyr Ile Val Leu Leu Pro Glu Ser Ile Pro Phe Leu Ala Glu Leu Met
        2100                    2105                    2110
gaa gat gaa tgt gaa gaa gta gaa cat cag tgc caa aag act att cag      6502
Glu Asp Glu Cys Glu Glu Val Glu His Gln Cys Gln Lys Thr Ile Gln
2115                    2120                    2125                    2130
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Gln Leu Glu Thr Val Leu Gly Glu Pro Leu Gln Ser Tyr Phe   *
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gcactttggg aggccgaggc agatggatca cgaggtcagg agttcgagac cagcctggac      660
aacatagtga aaccctgtct ctactaaaaa tacaaaaatt agccaggagc ggtggcaggc      720
gcctgtagtc ccagctactt tggaggctga gacaggagaa tcgcttgaac ctgggaggcg      780
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tgtaa                                                                  845


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Asp Ala Ser Leu Leu Ser Arg Asp Glu Val Ala Ser Leu Leu Phe Asp
            20                  25                  30
Pro Lys Glu Ala Ala Thr Ile Asp Arg Asp Thr Ala Phe Ala Ile Gly
            35                  40                  45
Cys Thr Gly Leu Glu Glu Leu Leu Gly Ile Asp Pro Ser Phe Glu Gln
        50                  55                  60
Phe Glu Ala Pro Leu Phe Ser Gln Leu Ala Lys Thr Leu Glu Arg Ser
65                  70                  75                  80
Val Gln Thr Lys Ala Val Asn Lys Gln Leu Asp Glu Asn Ile Ser Leu
                85                  90                  95
Phe Leu Ile His Leu Ser Pro Tyr Phe Leu Leu Lys Pro Ala Gln Lys
                100                 105                 110
Cys Leu Glu Trp Leu Ile His Arg Phe His Ile His Leu Tyr Asn Gln
            115                 120                 125
Asp Ser Leu Ile Ala Cys Val Leu Pro Tyr His Glu Thr Arg Ile Phe
            130                 135                 140
Val Arg Val Ile Gln Leu Leu Lys Ile Asn Asn Ser Lys His Arg Trp
145                 150                 155                 160
Phe Trp Leu Leu Pro Val Lys Gln Ser Gly Val Pro Leu Ala Lys Gly
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                    165                    170                    175
Thr Leu Ile Thr His Cys Tyr Lys Asp Leu Gly Phe Met Asp Phe Ile
            180                    185                    190
Cys Ser Leu Val Thr Lys Ser Val Lys Val Phe Ala Glu Tyr Pro Gly
            195                    200                    205
Ser Ser Ala Gln Leu Arg Val Leu Leu Ala Phe Tyr Ala Ser Thr Ile
210                    215                    220
Val Ser Ala Leu Val Ala Ala Glu Asp Val Ser Asp Asn Ile Ile Ala
225                    230                    235                    240
Lys Leu Phe Pro Tyr Ile Gln Lys Gly Leu Lys Ser Ser Leu Pro Asp
                    245                    250                    255
Tyr Arg Ala Ala Thr Tyr Met Ile Ile Cys Gln Ile Ser Val Lys Val
            260                    265                    270
Thr Met Glu Asn Thr Phe Val Asn Ser Leu Ala Ser Gln Ile Ile Lys
            275                    280                    285
Thr Leu Thr Lys Ile Pro Ser Leu Ile Lys Asp Gly Leu Ser Cys Leu
            290                    295                    300
Ile Val Leu Leu Gln Arg Gln Lys Pro Glu Ser Leu Gly Lys Lys Pro
305                    310                    315                    320
Phe Pro His Leu Cys Asn Val Pro Asp Leu Ile Thr Ile Leu His Gly
                    325                    330                    335
Ile Ser Glu Thr Tyr Asp Val Ser Pro Leu Leu Arg Tyr Met Leu Pro
            340                    345                    350
His Leu Val Val Ser Ile Ile His His Val Thr Gly Glu Glu Thr Glu
            355                    360                    365
Gly Met Asp Gly Gln Ile Tyr Lys Arg His Leu Glu Ala Ile Leu Thr
            370                    375                    380
Lys Ile Ser Leu Lys Asn Asn Leu Asp His Leu Leu Ala Ser Leu Leu
385                    390                    395                    400
Phe Glu Glu Tyr Ile Ser Tyr Ser Ser Gln Glu Glu Met Asp Ser Asn
                    405                    410                    415
Lys Val Ser Leu Leu Asn Glu Gln Phe Leu Pro Leu Ile Arg Leu Leu
            420                    425                    430
Glu Ser Lys Tyr Pro Arg Thr Leu Asp Val Val Leu Glu Glu His Leu
            435                    440                    445
Lys Glu Ile Ala Asp Leu Lys Lys Gln Glu Leu Phe His Gln Phe Val
            450                    455                    460
Ser Leu Ser Thr Ser Gly Gly Lys Tyr Gln Phe Leu Ala Asp Ser Asp
465                    470                    475                    480
Thr Ser Leu Met Leu Ser Leu Asn His Pro Leu Ala Pro Val Arg Ile
                    485                    490                    495
Leu Ala Met Asn His Leu Lys Lys Ile Met Lys Thr Ser Lys Glu Gly
            500                    505                    510
Val Asp Glu Ser Phe Ile Lys Glu Ala Val Leu Ala Arg Leu Gly Asp
            515                    520                    525
Asp Asn Ile Asp Val Val Leu Ser Ala Ile Ser Ala Phe Glu Ile Phe
            530                    535                    540
Lys Glu His Phe Ser Ser Glu Val Thr Ile Ser Asn Leu Leu Asn Leu
545                    550                    555                    560
Phe Gln Arg Ala Glu Leu Ser Lys Asn Gly Glu Trp Tyr Glu Val Leu
                    565                    570                    575
Lys Ile Ala Ala Asp Ile Leu Ile Lys Glu Glu Ile Leu Ser Glu Asn
            580                    585                    590
Asp Gln Leu Ser Asn Gln Val Val Val Cys Leu Leu Pro Phe Val Val
            595                    600                    605
Ile Asn Asp Asp Thr Glu Ser Ala Glu Met Lys Ile Ala Ile Tyr
            610                    615                    620
Leu Ser Lys Ser Gly Ile Cys Ser Leu His Pro Leu Leu Arg Gly Trp
625                    630                    635                    640
Glu Glu Ala Leu Glu Asn Val Ile Lys Ser Thr Lys Pro Gly Lys Leu
                    645                    650                    655
Ile Gly Val Ala Asn Gln Lys Met Ile Glu Leu Leu Ala Asp Asn Ile
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Asn Leu Gly Asp Pro Ser Ser Met Leu Lys Met Val Glu Asp Leu Ile
         675                    680                    685
Ser Val Gly Glu Glu Glu Ser Phe Asn Leu Lys Gln Lys Val Thr Phe
         690                    695                    700
His Val Ile Leu Ser Val Leu Val Ser Cys Cys Ser Ser Leu Lys Glu
705                    710                    715                    720
Thr His Phe Pro Phe Ala Ile Arg Val Phe Ser Leu Leu Gln Lys Lys
                   725                    730                    735
Ile Lys Lys Leu Glu Ser Val Ile Thr Ala Val Glu Ile Pro Ser Glu
                   740                    745                    750
Trp His Ile Glu Leu Met Leu Asp Arg Gly Ile Pro Val Glu Leu Trp
              755                    760                    765
Ala His Tyr Val Glu Glu Leu Asn Ser Thr Gln Arg Val Ala Val Glu
         770                    775                    780
Asp Ser Val Phe Leu Val Phe Ser Leu Lys Lys Phe Ile Tyr Ala Leu
785                    790                    795                    800
Lys Ala Pro Lys Ser Phe Pro Lys Gly Asp Ile Trp Trp Asn Pro Glu
                   805                    810                    815
Gln Leu Lys Glu Asp Ser Arg Asp Tyr Leu His Leu Leu Ile Gly Leu
              820                    825                    830
Phe Glu Met Met Leu Asn Gly Ala Asp Ala Val His Phe Arg Val Leu
         835                    840                    845
Met Lys Leu Phe Ile Lys Val His Leu Glu Asp Val Phe Gln Leu Phe
         850                    855                    860
Lys Phe Cys Ser Val Leu Trp Thr Tyr Gly Ser Ser Leu Ser Asn Pro
865                    870                    875                    880
Leu Asn Cys Ser Val Lys Thr Val Leu Gln Thr Gln Ala Leu Tyr Val
                   885                    890                    895
Gly Cys Ala Met Leu Ser Ser Gln Lys Thr Gln Cys Lys His Gln Leu
                   900                    905                    910
Ala Ser Ile Ser Ser Pro Val Val Thr Ser Leu Leu Ile Asn Leu Gly
                   915                    920                    925
Ser Pro Val Lys Glu Val Arg Arg Ala Ala Ile Gln Cys Leu Gln Ala
         930                    935                    940
Leu Ser Gly Val Ala Ser Pro Phe Tyr Leu Ile Ile Asp His Leu Ile
945                    950                    955                    960
Ser Lys Ala Glu Glu Ile Thr Ser Asp Ala Ala Tyr Val Ile Gln Asp
                   965                    970                    975
Leu Ala Thr Leu Phe Glu Glu Leu Gln Arg Glu Lys Lys Leu Lys Ser
                   980                    985                    990
His Gln Lys Leu Ser Glu Thr Leu Lys Asn Leu Leu Ser Cys Val Tyr
                   995                    1000                   1005
Ser Cys Pro Ser Tyr Ile Ala Lys Asp Leu Met Lys Val Leu Gln Gly
         1010                   1015                   1020
Val Asn Gly Glu Met Val Leu Ser Gln Leu Leu Pro Met Ala Glu Gln
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Leu Leu Glu Lys Ile Gln Lys Glu Pro Thr Ala Val Leu Lys Asp Glu
                   1045                   1050                   1055
Ala Met Val Leu His Leu Thr Leu Gly Lys Tyr Asn Glu Phe Ser Val
                   1060                   1065                   1070
Ser Leu Leu Asn Glu Asp Pro Lys Ser Leu Asp Ile Phe Ile Lys Ala
         1075                   1080                   1085
Val His Thr Thr Lys Glu Leu Tyr Ala Gly Met Pro Thr Ile Gln Ile
         1090                   1095                   1100
Thr Ala Leu Glu Lys Ile Thr Lys Pro Phe Phe Ala Ala Ile Ser Asp
1105                   1110                   1115                   1120
Glu Lys Val Gln Gln Lys Leu Leu Arg Met Leu Phe Asp Leu Leu Val
                   1125                   1130                   1135
Asn Cys Lys Asn Ser His Cys Ala Gln Thr Val Ser Ser Val Phe Lys
         1140                   1145                   1150
Gly Ile Ser Val Asn Ala Glu Gln Val Arg Ile Glu Leu Glu Pro Pro

                              68
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Asp Lys Ala Lys Pro Leu Gly Thr Val Gln Gln Lys Arg Arg Gln Lys
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Met Gln Gln Lys Lys Ser Gln Asp Leu Glu Ser Val Gln Glu Val Gly
1185                1190                1195                    1200
Gly Ser Tyr Trp Gln Arg Val Thr Leu Ile Leu Glu Leu Leu Gln His
                1205                1210                    1215
Lys Lys Lys Leu Arg Ser Pro Gln Ile Leu Val Pro Thr Leu Phe Asn
            1220                1225                    1230
Leu Leu Ser Arg Cys Leu Glu Pro Leu Pro Gln Glu Gln Gly Asn Met
            1235                1240                1245
Glu Tyr Thr Lys Gln Leu Ile Leu Ser Cys Leu Leu Asn Ile Cys Gln
        1250                1255                1260
Lys Leu Ser Pro Asp Gly Gly Lys Ile Pro Lys Asp Ile Leu Asp Glu
1265                1270                1275                    1280
Glu Lys Phe Asn Val Glu Leu Ile Val Gln Cys Ile Arg Leu Ser Glu
                1285                1290                    1295
Met Pro Gln Thr His His His Ala Leu Leu Leu Leu Gly Thr Val Ala
                1300                1305                    1310
Gly Ile Phe Pro Asp Lys Val Leu His Asn Ile Met Ser Ile Phe Thr
            1315                1320                1325
Phe Met Gly Ala Asn Val Met Arg Leu Asp Asp Thr Tyr Ser Phe Gln
            1330                1335                1340
Val Ile Asn Lys Thr Val Lys Met Val Ile Pro Ala Leu Ile Gln Ser
1345                1350                1355                    1360
Asp Ser Gly Asp Ser Ile Glu Val Ser Arg Asn Val Glu Glu Ile Val
                1365                1370                    1375
Val Lys Ile Ile Ser Val Phe Val Asp Ala Leu Pro His Val Pro Glu
            1380                1385                1390
His Arg Arg Leu Pro Ile Leu Val Gln Leu Val Asp Thr Leu Gly Ala
            1395                1400                1405
Glu Lys Phe Leu Trp Ile Leu Leu Ile Leu Leu Phe Glu Gln Tyr Val
        1410                1415                1420
Thr Lys Thr Val Leu Ala Ala Ala Tyr Gly Glu Lys Asp Ala Ile Leu
1425                1430                1435                    1440
Glu Ala Asp Thr Glu Phe Trp Phe Ser Val Cys Cys Glu Phe Ser Val
                1445                1450                    1455
Gln His Gln Ile Gln Ser Leu Met Asn Ile Leu Gln Tyr Leu Leu Lys
            1460                1465                1470
Leu Pro Glu Glu Lys Glu Glu Thr Ile Pro Lys Ala Val Ser Phe Asn
            1475                1480                1485
Lys Ser Glu Ser Gln Glu Glu Met Leu Gln Val Phe Asn Val Glu Thr
        1490                1495                1500
His Thr Ser Lys Gln Leu Arg His Phe Lys Phe Leu Ser Val Ser Phe
1505                1510                1515                    1520
Met Ser Gln Leu Leu Ser Ser Asn Asn Phe Leu Lys Lys Val Val Glu
                1525                1530                    1535
Ser Gly Gly Pro Glu Ile Leu Lys Gly Leu Glu Glu Arg Leu Leu Glu
            1540                1545                1550
Thr Val Leu Gly Tyr Ile Ser Ala Val Ala Gln Ser Met Glu Arg Asn
        1555                1560                1565
Ala Asp Lys Leu Thr Val Lys Phe Trp Arg Ala Leu Leu Ser Lys Ala
        1570                1575                1580
Tyr Asp Leu Leu Asp Lys Val Asn Ala Leu Leu Pro Thr Glu Thr Phe
1585                1590                1595                    1600
Ile Pro Val Ile Arg Gly Leu Val Gly Asn Pro Leu Pro Ser Val Arg
                1605                1610                    1615
Arg Lys Ala Leu Asp Leu Leu Asn Asn Lys Leu Gln Gln Asn Ile Ser
            1620                1625                1630
Trp Lys Lys Thr Ile Val Thr Arg Phe Leu Lys Leu Val Pro Asp Leu
            1635                1640                1645
Leu Ala Ile Val Gln Arg Lys Lys Lys Glu Gly Glu Glu Glu Gln Ala
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Ile Asn Arg Gln Thr Ala Leu Tyr Thr Leu Lys Leu Leu Cys Lys Asn
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Phe Gly Ala Glu Asn Pro Asp Pro Phe Val Pro Val Leu Xaa Thr Ala
                       1685                    1690                    1695
Val Lys Leu Ile Ala Pro Glu Arg Lys Glu Glu Lys Asn Val Leu Gly
                       1700                    1705                    1710
Ser Ala Leu Leu Cys Ile Ala Glu Val Thr Ser Thr Leu Glu Ala Leu
              1715                    1720                    1725
Ala Ile Pro Gln Leu Pro Ser Leu Met Pro Ser Leu Leu Thr Thr Met
              1730                    1735                    1740
Lys Asn Thr Ser Glu Leu Val Ser Ser Glu Val Tyr Leu Leu Ser Ala
1745                    1750                    1755                    1760
Leu Ala Ala Leu Gln Lys Val Val Glu Thr Leu Pro His Phe Ile Ser
                       1765                    1770                    1775
Pro Tyr Leu Glu Gly Ile Leu Ser Gln Val Ile His Leu Glu Lys Ile
                       1780                    1785                    1790
Thr Ser Glu Met Gly Ser Ala Ser Gln Ala Asn Ile Arg Leu Thr Ser
                       1795                    1800                    1805
Leu Lys Lys Thr Leu Ala Thr Thr Leu Ala Pro Arg Val Leu Leu Pro
              1810                    1815                    1820
Ala Ile Lys Lys Thr Tyr Lys Gln Ile Glu Lys Asn Trp Lys Asn His
1825                    1830                    1835                    1840
Met Gly Pro Phe Met Ser Ile Leu Gln Glu His Ile Gly Xaa Met Lys
                       1845                    1850                    1855
Lys Glu Glu Leu Thr Ser His Gln Ser Gln Leu Thr Ala Phe Phe Leu
              1860                    1865                    1870
Glu Ala Leu Asp Phe Arg Ala Gln His Ser Glu Asn Asp Leu Glu Glu
              1875                    1880                    1885
Val Gly Lys Thr Glu Asn Cys Ile Ile Asp Cys Leu Val Ala Met Val
              1890                    1895                    1900
Val Lys Leu Ser Glu Val Thr Phe Arg Pro Leu Phe Phe Lys Leu Phe
1905                    1910                    1915                    1920
Asp Trp Ala Lys Thr Glu Asp Ala Pro Lys Asp Arg Leu Leu Thr Phe
                       1925                    1930                    1935
Tyr Asn Leu Ala Asp Cys Ile Ala Glu Lys Leu Lys Gly Leu Phe Thr
              1940                    1945                    1950
Leu Phe Ala Gly His Leu Val Lys Pro Phe Ala Asp Thr Leu Xaa Gln
              1955                    1960                    1965
Val Asn Ile Ser Lys Thr Asp Glu Ala Phe Phe Asp Ser Glu Asn Asp
              1970                    1975                    1980
Pro Glu Lys Cys Cys Leu Leu Leu Gln Phe Ile Leu Asn Cys Leu Tyr
1985                    1990                    1995                    2000
Lys Ile Phe Leu Phe Asp Thr Gln His Phe Ile Ser Lys Glu Arg Ala
              2005                    2010                    2015
Xaa Ala Leu Met Met Pro Leu Val Asp Gln Leu Glu Asn Arg Leu Gly
              2020                    2025                    2030
Gly Glu Glu Lys Phe Gln Glu Arg Val Thr Lys His Leu Ile Pro Cys
              2035                    2040                    2045
Ile Ala Gln Phe Ser Val Ala Met Ala Asp Asp Ser Leu Trp Lys Pro
              2050                    2055                    2060
Leu Asn Tyr Gln Ile Leu Leu Lys Thr Arg Asp Ser Ser Pro Lys Val
2065                    2070                    2075                    2080
Arg Phe Ala Ala Leu Ile Thr Val Leu Ala Leu Ala Glu Lys Leu Lys
                       2085                    2090                    2095
Glu Asn Tyr Ile Val Leu Leu Pro Glu Ser Ile Pro Phe Leu Ala Glu
              2100                    2105                    2110
Leu Met Glu Asp Glu Cys Glu Glu Val Glu His Gln Cys Gln Lys Thr
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Ile Gln Gln Leu Glu Thr Val Leu Gly Glu Pro Leu Gln Ser Tyr Phe
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70

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acctttaaat gaaacttgcc taaaatctta ggtcatacac agaagagact ccaatcgaca     180
agaagctgga aaagaatg atg ttg tcc tta aac aac cta cag aat atc atc      231
                    Met Leu Ser Leu Asn Asn Leu Gln Asn Ile Ile
                     1               5                  10
tat aac ccg gta atc ccg tat gtt ggc acc att ccc gat cag ctg gat     279
Tyr Asn Pro Val Ile Pro Tyr Val Gly Thr Ile Pro Asp Gln Leu Asp
            15                  20                  25
cct gga act ttg att gtg ata tgt ggg cat gtt cct agt gac gca gac     327
Pro Gly Thr Leu Ile Val Ile Cys Gly His Val Pro Ser Asp Ala Asp
                30                  35                  40
aga ttc cag gtg gat ctg cag aat ggc agc agt gtg aaa cct cga gcc     375
Arg Phe Gln Val Asp Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala
        45                  50                  55
gat gtg gcc ttt cat ttc aat cct cgt ttc aaa agg gcc ggc tgc att     423
Asp Val Ala Phe His Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile
60                  65                  70                  75
gtt tgc aat act ttg ata aat gaa aaa tgg gga cgg gaa gag atc acc     471
Val Cys Asn Thr Leu Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr
                80                  85                  90
tat gac acg cct ttc aaa aga gaa aag tct ttt gag atc gtg att atg     519
Tyr Asp Thr Pro Phe Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met
                95                 100                 105
gtg cta aag gac aaa ttc cag gtg gct gta aat gga aaa cat act ctg     567
Val Leu Lys Asp Lys Phe Gln Val Ala Val Asn Gly Lys His Thr Leu
            110                 115                 120
ctc tat ggc cac agg atc ggc cca gag aaa ata gac act ctg ggc att     615
Leu Tyr Gly His Arg Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile
            125                 130                 135
tat ggc aaa gtg aat att cac tca att ggt ttt agc ttc agc tcg gac     663
Tyr Gly Lys Val Asn Ile His Ser Ile Gly Phe Ser Phe Ser Ser Asp
140                 145                 150                 155
tta caa agt acc caa gca tct agt ctg gaa ctg aca gag ata agt aga     711
Leu Gln Ser Thr Gln Ala Ser Ser Leu Glu Leu Thr Glu Ile Ser Arg
                160                 165                 170
gaa aat gtt cca aag tct ggc acg ccc cag ctt agc ctg cca ttc gct     759
Glu Asn Val Pro Lys Ser Gly Thr Pro Gln Leu Ser Leu Pro Phe Ala
            175                 180                 185
gca agg ttg aac acc ccc atg ggc cct gga cga act gtc gtc gtt aaa     807
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Ala Arg Leu Asn Thr Pro Met Gly Pro Gly Arg Thr Val Val Val Lys
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gga gaa gtg aat gca aat gcc aaa agc ttt aat gtt gac cta cta gca   855
Gly Glu Val Asn Ala Asn Ala Lys Ser Phe Asn Val Asp Leu Leu Ala
    205                 210                 215
gga aaa tca aag gat att gct cta cac ttg aac cca cgc ctg aat att   903
Gly Lys Ser Lys Asp Ile Ala Leu His Leu Asn Pro Arg Leu Asn Ile
220             225                 230                 235
aaa gca ttt gta aga aat tct ttt ctt cag gag tcc tgg gga gaa gaa   951
Lys Ala Phe Val Arg Asn Ser Phe Leu Gln Glu Ser Trp Gly Glu Glu
                240                 245                 250
gag aga aat att acc tct ttc cca ttt agt cct ggg atg tac ttt gag   999
Glu Arg Asn Ile Thr Ser Phe Pro Phe Ser Pro Gly Met Tyr Phe Glu
            255                 260                 265
atg ata att tac tgt gat gtt aga gaa ttc aag gtt gca gta aat ggc  1047
Met Ile Ile Tyr Cys Asp Val Arg Glu Phe Lys Val Ala Val Asn Gly
        270                 275                 280
gta cac agc ctg gag tac aaa cac aga ttt aaa gag ctc agc agt att  1095
Val His Ser Leu Glu Tyr Lys His Arg Phe Lys Glu Leu Ser Ser Ile
        285                 290                 295
gac acg ctg gaa att aat gga gac atc cac tta ctg gaa gta agg agc  1143
Asp Thr Leu Glu Ile Asn Gly Asp Ile His Leu Leu Glu Val Arg Ser
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Trp  *
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acctttaaat gaaacttgcc taaaatctta ggtcatacac agaagagact ccaatcgaca    180
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               Met Leu Ser Leu Asn Asn Leu Gln Asn Ile Ile
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73

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Tyr Asn Pro Val Ile Pro Tyr Val Gly Thr Ile Pro Asp Gln Leu Asp
            15                      20                      25
cct gga act ttg att gtg ata tgt ggg cat gtt cct agt gac gca gac      327
Pro Gly Thr Leu Ile Val Ile Cys Gly His Val Pro Ser Asp Ala Asp
            30                      35                      40
aga ttc cag gtg gat ctg cag aat ggc agc agt gtg aaa cct cga gcc      375
Arg Phe Gln Val Asp Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala
            45                      50                      55
gat gtg gcc ttt cat ttc aat cct cgt ttc aaa agg gcc ggc tgc att      423
Asp Val Ala Phe His Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile
60                      65                      70                      75
gtt tgc aat act ttg ata aat gaa aaa tgg gga cgg gaa gag atc acc      471
Val Cys Asn Thr Leu Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr
            80                      85                      90
tat gac acg cct ttc aaa aga gaa aag tct ttt gag atc gtg att atg      519
Tyr Asp Thr Pro Phe Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met
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gtg cta aag gac aaa ttc cag gtg gct gta aat gga aaa cat act ctg      567
Val Leu Lys Asp Lys Phe Gln Val Ala Val Asn Gly Lys His Thr Leu
            110                     115                     120
ctc tat ggc cac agg atc ggc cca gag aaa ata gac act ctg ggc att      615
Leu Tyr Gly His Arg Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile
            125                     130                     135
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Tyr Gly Lys Val Asn Ile His Ser Ile Gly Phe Ser Phe Ser Ser Asp
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tta caa agt acc caa gca tct agt ctg gaa ctg aca gag ata agt aga      711
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Glu Asn Val Pro Lys Ser Gly Thr Pro Gln Leu Pro Ser Asn Arg Gly
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gga gac att tct aaa atc gca ccc aga act gtc tac acc aag agc aaa      807
Gly Asp Ile Ser Lys Ile Ala Pro Arg Thr Val Tyr Thr Lys Ser Lys
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Asp Ser Thr Val Asn His Thr Leu Thr Cys Thr Lys Ile Pro Pro Met
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aac tat gtg tca aag agc ctg cca ttc gct gca agg ttg aac acc ccc      903
Asn Tyr Val Ser Lys Ser Leu Pro Phe Ala Ala Arg Leu Asn Thr Pro
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gcc aaa agc ttt aat gtt gac cta cta gca gga aaa tca aag gat att      999
Ala Lys Ser Phe Asn Val Asp Leu Leu Ala Gly Lys Ser Lys Asp Ile
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gct cta cac ttg aac cca cgc ctg aat att aaa gca ttt gta aga aat      1047
Ala Leu His Leu Asn Pro Arg Leu Asn Ile Lys Ala Phe Val Arg Asn
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tct ttt ctt cag gag tcc tgg gga gaa gaa gag aga aat att acc tct      1095
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            285                     290                     295
ttc cca ttt agt cct ggg atg tac ttt gag atg ata att tac tgt gat      1143
Phe Pro Phe Ser Pro Gly Met Tyr Phe Glu Met Ile Ile Tyr Cys Asp
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Val Arg Glu Phe Lys Val Ala Val Asn Gly Val His Ser Leu Glu Tyr
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aaa cac aga ttt aaa gag ctc agc agt att gac acg ctg gaa att aat      1239
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74

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Gly Asp Ile His Leu Leu Glu Val Arg Ser Trp  *
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75

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agaagctgga aaagaatg atg ttg tcc tta aac aac cta cag aat atc atc       231
                    Met Leu Ser Leu Asn Asn Leu Gln Asn Ile Ile
                     1               5                   10
tat aac ccg gta atc ccg tat gtt ggc acc att ccc gat cag ctg gat      279
Tyr Asn Pro Val Ile Pro Tyr Val Gly Thr Ile Pro Asp Gln Leu Asp
            15                  20                  25
cct gga act ttg att gtg ata tgt ggg cat gtt cct agt gac gca gac      327
Pro Gly Thr Leu Ile Val Ile Cys Gly His Val Pro Ser Asp Ala Asp
            30                  35                  40
aga ttc cag gtg gat ctg cag aat ggc agc agt gtg aaa cct cga gcc      375
Arg Phe Gln Val Asp Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala
            45                  50                  55
gat gtg gcc ttt cat ttc aat cct cgt ttc aaa agg gcc ggc tgc att      423
Asp Val Ala Phe His Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile
60                  65                  70                  75
gtt tgc aat act ttg ata aat gaa aaa tgg gga cgg gaa gag atc acc      471
Val Cys Asn Thr Leu Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr
                    80                  85                  90
tat gac acg cct ttc aaa aga gaa aag tct ttt gag atc gtg att atg      519
Tyr Asp Thr Pro Phe Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met
                95                  100                 105
gtg cta aag gac aaa ttc cag gtg gct gta aat gga aaa cat act ctg      567
Val Leu Lys Asp Lys Phe Gln Val Ala Val Asn Gly Lys His Thr Leu
            110                 115                 120
ctc tat ggc cac agg atc ggc cca gag aaa ata gac act ctg ggc att      615
Leu Tyr Gly His Arg Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile
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76

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Leu Gln Ser Thr Gln Ala Ser Ser Leu Glu Leu Thr Glu Ile Ser Arg
                        160                    165                    170
gaa aat gtt cca aag tct ggc acg ccc cag ctt agc ctg cca ttc gct    759
Glu Asn Val Pro Lys Ser Gly Thr Pro Gln Leu Ser Leu Pro Phe Ala
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gca agg ttg aac acc ccc atg ggc cct gga cga act gtc gtc gtt aaa    807
Ala Arg Leu Asn Thr Pro Met Gly Pro Gly Arg Thr Val Val Val Lys
        190                    195                    200
gga gaa gtg aat gca aat gcc aaa agc ttt aat gtt gac cta cta gca    855
Gly Glu Val Asn Ala Asn Ala Lys Ser Phe Asn Val Asp Leu Leu Ala
        205                    210                    215
gga aaa tca aag gat att gct cta cac ttg aac cca cgc ctg aat att    903
Gly Lys Ser Lys Asp Ile Ala Leu His Leu Asn Pro Arg Leu Asn Ile
220                    225                    230                    235
aaa gca ttt gta aga aat tct ttt ctt cag gag tcc tgg gga gaa gaa    951
Lys Ala Phe Val Arg Asn Ser Phe Leu Gln Glu Ser Trp Gly Glu Glu
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Glu Arg Asn Ile Thr Ser Phe Pro Phe Ser Pro Gly Met Tyr Phe Glu
                255                    260                    265
atg ata att tac tgt gat gtt aga gaa ttc aag gtt gca gta aat ggc    1047
Met Ile Ile Tyr Cys Asp Val Arg Glu Phe Lys Val Ala Val Asn Gly
                270                    275                    280
gta cac agc ctg gag tac aaa cac aga ttt aaa gag ctc agc agt att    1095
Val His Ser Leu Glu Tyr Lys His Arg Phe Lys Glu Leu Ser Ser Ile
        285                    290                    295
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Asp Thr Leu Glu Ile Asn Gly Asp Ile His Leu Leu Glu Gln Ser Phe
300                    305                    310                    315
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Asn Gln Lys Ser Glu Met Lys His Ile Asn Lys Ala Gly Gly Ala Thr
                320                    325                    330
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Gly Leu His Trp Lys Leu Asn Lys Asn Pro Gln Asn Ser Asn Phe Leu
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77

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<213> Homo sapiens


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aacctgctcc gtggagcgcc tgaaacacca gtctttgggg ccagtgcctc agtttcaatc     300
caggtaacct ttaaatgaaa cttgcctaaa atcttaggtc atacacagaa gagactccaa     360
tcgacaagaa gctggaaaag aatg atg ttg tcc tta aac aac cta cag aat       411
                           Met Leu Ser Leu Asn Asn Leu Gln Asn
                           1                   5
atc atc tat aac ccg gta atc ccg tat gtt ggc acc att ccc gat cag       459
Ile Ile Tyr Asn Pro Val Ile Pro Tyr Val Gly Thr Ile Pro Asp Gln
10                  15                  20                  25
ctg gat cct gga act ttg att gtg ata tgt ggg cat gtt cct agt gac       507
Leu Asp Pro Gly Thr Leu Ile Val Ile Cys Gly His Val Pro Ser Asp
                    30                  35                  40
gca gac ag                                                            515
Ala Asp


<210> 11
<211> 304
<212> DNA
<213> Homo sapiens


<220>
<221> 5'UTR
<222> 1..173


<220>
<221> CDS
<222> 174..304


<400> 11
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ttctagaagc ttgtttctcc cacctgaaaa gactggattt gggacatgat cctgtagaac      60
ttcggagggc cagtgcctca gtttcaatcc aggtaacctt taaatgaaac ttgcctaaaa     120
tcttaggtca tacacagaag agactccaat cgacaagaag ctggaaaaga atg atg        176
                                                         Met
                                                         1

ttg tcc tta aac aac cta cag aat atc atc tat aac ccg gta atc ccg      224
Leu Ser Leu Asn Asn Leu Gln Asn Ile Ile Tyr Asn Pro Val Ile Pro
                5                   10                  15

tat gtt ggc acc att ccc gat cag ctg gat cct gga act ttg att gtg      272
Tyr Val Gly Thr Ile Pro Asp Gln Leu Asp Pro Gly Thr Leu Ile Val
            20                  25                  30

ata tgt ggg cat gtt cct agt gac gca gac ag                           304
Ile Cys Gly His Val Pro Ser Asp Ala Asp
    35                  40
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<210> 12
<211> 473
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..342

<220>
<221> CDS
<222> 343..473

<400> 12

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ttctagaagc ttgtttctcc cacctgaaaa gactggattt gggacatgat cctgtagaac      60
ttcggagatt ggggaagata atcggaagag gtaaaagaca ccgtccatga cacttcctgg     120
ggaagcagat gtatgtataa ggatccgccc acggacgcca gagccgggaa ccctgacggc     180
acttagctgc tgacaaacaa cctgctccgt ggagcgcctg aaacaccagt ctttggggcc     240
agtgcctcag tttcaatcca ggtaaccttt aaatgaaact tgcctaaaat cttaggtcat     300
acacagaaga gactccaatc gacaagaagc tggaaaagaa tg atg ttg tcc tta       354
                                               Met Leu Ser Leu
                                               1

aac aac cta cag aat atc atc tat aac ccg gta atc ccg tat gtt ggc      402
Asn Asn Leu Gln Asn Ile Ile Tyr Asn Pro Val Ile Pro Tyr Val Gly
5                   10                  15                  20

acc att ccc gat cag ctg gat cct gga act ttg att gtg ata tgt ggg      450
Thr Ile Pro Asp Gln Leu Asp Pro Gly Thr Leu Ile Val Ile Cys Gly
                25                  30                  35

cat gtt cct agt gac gca gac ag                                       473
His Val Pro Ser Asp Ala Asp
                40
```

<210> 13
<211> 2077
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..265

<220>
<221> CDS
<222> 266..913

<220>
<221> 3'UTR

<222> 914..2077

<400> 13

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ttctagaagc ttgtttctcc cacctgaaaa gactggattt gggacatgat cctgtagaac        50
ttcggagccg cccacggacg ccagagccgg gaaccctgac ggcacttagc tgctgacaaa       120
caacctgctc cgtggagcgc ctgaaacacc agtctttggg gccagtgcct cagtttcaat       180
ccaggtaacc tttaaatgaa acttgcctaa aatcttaggt catacacaga agagactcca       240
atcgacaaga agctggaaaa gaatg atg ttg tcc tta aac aac cta cag aat         292
                             Met Leu Ser Leu Asn Asn Leu Gln Asn
                             1               5
atc atc tat aac ccg gta atc ccg tat gtt ggc acc att ccc gat cag        340
Ile Ile Tyr Asn Pro Val Ile Pro Tyr Val Gly Thr Ile Pro Asp Gln
10                  15                  20                  25
ctg gat cct gga act ttg att gtg ata tgt ggg cat gtt cct agt gac       388
Leu Asp Pro Gly Thr Leu Ile Val Ile Cys Gly His Val Pro Ser Asp
                30                  35                  40
gca gac aga ttc cag gtg gat ctg cag aat ggc agc agt gtg aaa cct      436
Ala Asp Arg Phe Gln Val Asp Leu Gln Asn Gly Ser Ser Val Lys Pro
                45                  50                  55
cga gcc gat gtg gcc ttt cat ttc aat cct cgt ttc aaa agg gcc ggc      484
Arg Ala Asp Val Ala Phe His Phe Asn Pro Arg Phe Lys Arg Ala Gly
            60                  65                  70
tgc att gtt tgc aat act ttg ata aat gaa aaa tgg gga cgg gaa gag      532
Cys Ile Val Cys Asn Thr Leu Ile Asn Glu Lys Trp Gly Arg Glu Glu
        75                  80                  85
atc acc tat gac acg cct ttc aaa aga gaa aag tct ttt gag atc gtg      580
Ile Thr Tyr Asp Thr Pro Phe Lys Arg Glu Lys Ser Phe Glu Ile Val
90                  95                  100                 105
att atg gtg cta aag gac aaa ttc cag atg ata att tac tgt gat gtt      628
Ile Met Val Leu Lys Asp Lys Phe Gln Met Ile Ile Tyr Cys Asp Val
                110                 115                 120
aga gaa ttc aag gtt gca gta aat ggc gta cac agc ctg gag tac aaa      676
Arg Glu Phe Lys Val Ala Val Asn Gly Val His Ser Leu Glu Tyr Lys
                125                 130                 135
cac aga ttt aaa gag ctc agc agt att gac acg ctg gaa att aat gga      724
His Arg Phe Lys Glu Leu Ser Ser Ile Asp Thr Leu Glu Ile Asn Gly
                140                 145                 150
gac atc cac tta ctg gaa caa tca ttc aat caa aag agt gaa atg aag      772
Asp Ile His Leu Leu Glu Gln Ser Phe Asn Gln Lys Ser Glu Met Lys
            155                 160                 165
cac att aac aaa gca gga ggc gcc acg gac cgc ctc cct cca cac cgc      820
His Ile Asn Lys Ala Gly Gly Ala Thr Asp Arg Leu Pro Pro His Arg
170                 175                 180                 185
tcc ttc cgc ctt cat tcc ttg ccc aca ggc ttg cac tgg aag ctg aat      868
Ser Phe Arg Leu His Ser Leu Pro Thr Gly Leu His Trp Lys Leu Asn
                190                 195                 200
aag aat ccc caa aac tca aac ttc cta ggg atg cca ccc ctt tag        913
Lys Asn Pro Gln Asn Ser Asn Phe Leu Gly Met Pro Pro Leu  *
                205                 210                 215
tagctcacac ctcccccctc caagagctaa gaaacaaagg agaatgtact tttgtagctt      973
agataagcaa tgaatcagta aaggactgat ctacttgctc caccacccct cccttaataa     1033
taacatttac tgttatttcc tgggcctaag acttatgttc cagaactgtc acagctcccc     1093
atgtcacacc cactagcttg tgatctttgt caaataactg aaatctttta agcctctagt     1153
ttcttccttt gtaaacaga gataaaatgt tgtggttttt aagtgagata atccaagtaa      1213
agcacctaac atggagtagt gaatgaacat cggttgctac taaaagtgga catcctaccg     1273
catccttaat gccactaggc atttccatac aatctgggga ccaaaacttc aatcatataa     1333
atgtatgagg ttaattaaaa acactactgt aatctgcttg tatgatcaca aaccaccaca     1393
aaagaaaga tcgtgaagat tacactgtaa acggactctc aaatgatcag gaggtggtca      1453
cttcgcaact tgctccctcc acccaactca aaacaggagc tcgagcctgc ctgtatttga     1513
gactggagct gcctgtatga ggactggatc aactgctagt cacgttatat ccaaatctgc     1573
attatcattg ggcacatttt cacagaattt tactgaatta ttccttaatt gtttaatggt     1633
tgggaatagt ttgggaatta ccttccatca actctgctaa gaaaggaatg gattctggta     1693
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80

```
gcaagacaat ataattctcc tttagttttt cagccagtgc taacacagta atcaaagcag   1753
caaatcgaac ctgaaaggga taaaagagca aagaaataaa aagtagtgtt actgtattta   1813
ttatcttaag agctgtactg acttgagaca agctctaact ttttaaacat tagttcacac   1873
gcgtttattc acttcattat gttcattaag ctttcatctt agaataccag tttcaccatt   1933
tgggagctgt ttgtaatatg tgcaacctta taaatagtgt tttccaaact gtgtcccagg   1993
actgcaaatc tttaatgtga aatgtctttt tataatctct tcctttaaaa aaaaccaata   2053
aaataaaatg ccacatgcaa actc                                          2077
```

<210> 14
<211> 316
<212> PRT
<213> Homo sapiens

<400> 14

```
Met Leu Ser Leu Asn Asn Leu Gln Asn Ile Ile Tyr Asn Pro Val Ile
1               5                   10                  15
Pro Tyr Val Gly Thr Ile Pro Asp Gln Leu Asp Pro Gly Thr Leu Ile
                20                  25                  30
Val Ile Cys Gly His Val Pro Ser Asp Ala Asp Arg Phe Gln Val Asp
                35                  40                  45
Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala Asp Val Ala Phe His
        50                  55                  60
Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile Val Cys Asn Thr Leu
65                  70                  75                  80
Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr Tyr Asp Thr Pro Phe
                85                  90                  95
Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met Val Leu Lys Asp Lys
                100                 105                 110
Phe Gln Val Ala Val Asn Gly Lys His Thr Leu Leu Tyr Gly His Arg
            115                 120                 125
Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile Tyr Gly Lys Val Asn
            130                 135                 140
Ile His Ser Ile Gly Phe Ser Phe Ser Ser Asp Leu Gln Ser Thr Gln
145                 150                 155                 160
Ala Ser Ser Leu Glu Leu Thr Glu Ile Ser Arg Glu Asn Val Pro Lys
                165                 170                 175
Ser Gly Thr Pro Gln Leu Ser Leu Pro Phe Ala Ala Arg Leu Asn Thr
                180                 185                 190
Pro Met Gly Pro Gly Arg Thr Val Val Val Lys Gly Glu Val Asn Ala
            195                 200                 205
Asn Ala Lys Ser Phe Asn Val Asp Leu Leu Ala Gly Lys Ser Lys Asp
        210                 215                 220
Ile Ala Leu His Leu Asn Pro Arg Leu Asn Ile Lys Ala Phe Val Arg
225                 230                 235                 240
Asn Ser Phe Leu Gln Glu Ser Trp Gly Glu Glu Glu Arg Asn Ile Thr
                245                 250                 255
Ser Phe Pro Phe Ser Pro Gly Met Tyr Phe Glu Met Ile Ile Tyr Cys
                260                 265                 270
Asp Val Arg Glu Phe Lys Val Ala Val Asn Gly Val His Ser Leu Glu
            275                 280                 285
Tyr Lys His Arg Phe Lys Glu Leu Ser Ser Ile Asp Thr Leu Glu Ile
            290                 295                 300
Asn Gly Asp Ile His Leu Leu Glu Val Arg Ser Trp
305                 310                 315
```

<210> 15
<211> 358
<212> PRT
<213> Homo sapiens

<400> 15

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Met Leu Ser Leu Asn Asn Leu Gln Asn Ile Ile Tyr Asn Pro Val Ile
```

81

```
1                   5                   10                  15
Pro Tyr Val Gly Thr Ile Pro Asp Gln Leu Asp Pro Gly Thr Leu Ile
            20                  25                  30
Val Ile Cys Gly His Val Pro Ser Asp Ala Asp Arg Phe Gln Val Asp
        35                  40                  45
Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala Asp Val Ala Phe His
        50                  55                  60
Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile Val Cys Asn Thr Leu
65                  70                  75                  80
Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr Tyr Asp Thr Pro Phe
                85                  90                  95
Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met Val Leu Lys Asp Lys
            100                 105                 110
Phe Gln Val Ala Val Asn Gly Lys His Thr Leu Leu Tyr Gly His Arg
        115                 120                 125
Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile Tyr Gly Lys Val Asn
    130                 135                 140
Ile His Ser Ile Gly Phe Ser Phe Ser Ser Asp Leu Gln Ser Thr Gln
145                 150                 155                 160
Ala Ser Ser Leu Glu Leu Thr Glu Ile Ser Arg Glu Asn Val Pro Lys
                165                 170                 175
Ser Gly Thr Pro Gln Leu Pro Ser Asn Arg Gly Gly Asp Ile Ser Lys
            180                 185                 190
Ile Ala Pro Arg Thr Val Tyr Thr Lys Ser Lys Asp Ser Thr Val Asn
        195                 200                 205
His Thr Leu Thr Cys Thr Lys Ile Pro Pro Met Asn Tyr Val Ser Lys
    210                 215                 220
Ser Leu Pro Phe Ala Ala Arg Leu Asn Thr Pro Met Gly Pro Gly Arg
225                 230                 235                 240
Thr Val Val Val Lys Gly Glu Val Asn Ala Asn Ala Lys Ser Phe Asn
                245                 250                 255
Val Asp Leu Leu Ala Gly Lys Ser Lys Asp Ile Ala Leu His Leu Asn
            260                 265                 270
Pro Arg Leu Asn Ile Lys Ala Phe Val Arg Asn Ser Phe Leu Gln Glu
        275                 280                 285
Ser Trp Gly Glu Glu Glu Arg Asn Ile Thr Ser Phe Pro Phe Ser Pro
    290                 295                 300
Gly Met Tyr Phe Glu Met Ile Ile Tyr Cys Asp Val Arg Glu Phe Lys
305                 310                 315                 320
Val Ala Val Asn Gly Val His Ser Leu Glu Tyr Lys His Arg Phe Lys
            325                 330                 335
Glu Leu Ser Ser Ile Asp Thr Leu Glu Ile Asn Gly Asp Ile His Leu
        340                 345                 350
Leu Glu Val Arg Ser Trp
        355


<210> 16
<211> 368
<212> PRT
<213> Homo sapiens

<400> 16
Met Leu Ser Leu Asn Asn Leu Gln Asn Ile Ile Tyr Asn Pro Val Ile
1                   5                   10                  15
Pro Tyr Val Gly Thr Ile Pro Asp Gln Leu Asp Pro Gly Thr Leu Ile
            20                  25                  30
Val Ile Cys Gly His Val Pro Ser Asp Ala Asp Arg Phe Gln Val Asp
        35                  40                  45
Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala Asp Val Ala Phe His
        50                  55                  60
Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile Val Cys Asn Thr Leu
65                  70                  75                  80
```

```
Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr Tyr Asp Thr Pro Phe
                85                      90                      95
Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met Val Leu Lys Asp Lys
            100                     105                     110
Phe Gln Val Ala Val Asn Gly Lys His Thr Leu Leu Tyr Gly His Arg
            115                     120                     125
Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile Tyr Gly Lys Val Asn
        130                     135                     140
Ile His Ser Ile Gly Phe Ser Phe Ser Ser Asp Leu Gln Ser Thr Gln
145                     150                     155                     160
Ala Ser Ser Leu Glu Leu Thr Glu Ile Ser Arg Glu Asn Val Pro Lys
                165                     170                     175
Ser Gly Thr Pro Gln Leu Ser Leu Pro Phe Ala Ala Arg Leu Asn Thr
                180                     185                     190
Pro Met Gly Pro Gly Arg Thr Val Val Val Lys Gly Glu Val Asn Ala
            195                     200                     205
Asn Ala Lys Ser Phe Asn Val Asp Leu Leu Ala Gly Lys Ser Lys Asp
        210                     215                     220
Ile Ala Leu His Leu Asn Pro Arg Leu Asn Ile Lys Ala Phe Val Arg
225                     230                     235                     240
Asn Ser Phe Leu Gln Glu Ser Trp Gly Glu Glu Glu Arg Asn Ile Thr
                245                     250                     255
Ser Phe Pro Phe Ser Pro Gly Met Tyr Phe Glu Met Ile Ile Tyr Cys
                260                     265                     270
Asp Val Arg Glu Phe Lys Val Ala Val Asn Gly Val His Ser Leu Glu
            275                     280                     285
Tyr Lys His Arg Phe Lys Glu Leu Ser Ser Ile Asp Thr Leu Glu Ile
            290                     295                     300
Asn Gly Asp Ile His Leu Leu Glu Gln Ser Phe Asn Gln Lys Ser Glu
305                     310                     315                     320
Met Lys His Ile Asn Lys Ala Gly Gly Ala Thr Asp Arg Leu Pro Pro
                325                     330                     335
His Arg Ser Phe Arg Leu His Ser Leu Pro Thr Gly Leu His Trp Lys
                340                     345                     350
Leu Asn Lys Asn Pro Gln Asn Ser Asn Phe Leu Gly Met Pro Pro Leu
                355                     360                     365
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<210> 17
<211> 215
<212> PRT
<213> Homo sapiens

<400> 17

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Met Leu Ser Leu Asn Asn Leu Gln Asn Ile Ile Tyr Asn Pro Val Ile
1               5                       10                      15
Pro Tyr Val Gly Thr Ile Pro Asp Gln Leu Asp Pro Gly Thr Leu Ile
            20                      25                      30
Val Ile Cys Gly His Val Pro Ser Asp Ala Asp Arg Phe Gln Val Asp
            35                      40                      45
Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala Asp Val Ala Phe His
        50                      55                      60
Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile Val Cys Asn Thr Leu
65                      70                      75                      80
Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr Tyr Asp Thr Pro Phe
                85                      90                      95
Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met Val Leu Lys Asp Lys
            100                     105                     110
Phe Gln Met Ile Ile Tyr Cys Asp Val Arg Glu Phe Lys Val Ala Val
            115                     120                     125
Asn Gly Val His Ser Leu Glu Tyr Lys His Arg Phe Lys Glu Leu Ser
        130                     135                     140
Ser Ile Asp Thr Leu Glu Ile Asn Gly Asp Ile His Leu Leu Glu Gln
```

```
145                    150                    155                    160
Ser Phe Asn Gln Lys Ser Glu Met Lys His Ile Asn Lys Ala Gly Gly
                165                    170                    175
Ala Thr Asp Arg Leu Pro Pro His Arg Ser Phe Arg Leu His Ser Leu
            180                    185                    190
Pro Thr Gly Leu His Trp Lys Leu Asn Lys Asn Pro Gln Asn Ser Asn
        195                    200                    205
Phe Leu Gly Met Pro Pro Leu
    210                    215
```

<210> 18
<211> 504
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 81
<223> 99-7177-81 : polymorphic base C or T

<220>
<221> misc_binding
<222> 69..93
<223> 99-7177-81.probe

<220>
<221> primer_bind
<222> 62..80
<223> 99-7177-81.mis

<220>
<221> primer_bind
<222> 82..100
<223> 99-7177-81.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-7177.pu

<220>
<221> primer_bind
<222> 484..504
<223> 99-7177.rp complement

<400> 18
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aatcctgacc caccttctcc caagcacgca tgtagaggaa agaaagcaag agcgatagct      60
gaggggatca gcctactaga yggaggcagg tgtttcaaga tggtgttgga agggcaagcc     120
gagaactcta gtagcgggga ggggaaaact aaaactttat tactgtaagc aaatatcaca     180
gcaaatcagc cttaagtagg tataaaagaa cccataaaag aagacaaaat gtaaccaaag     240
ctcaccagac cacagaagag tcatcactgg agtcggaaga cagacgcgct ggatcctgca     300
gtaggagttg gggcatcccc cagcatagga caacagcaac cttcaatcct ccttcgtata     360
agctcctttt attaagtcca attgttactt tgggcaccct ctgttgtttg ctggtgaggg     420
cccttcccca gcaagcaaca ctgaaacagt ggttctggga gcagcgtcct gggacgcgtt     480
ccaggacttg agttaatttc tggg                                            504
```

<210> 19
<211> 488
<212> DNA
<213> Homo sapiens

<220>

84

<221> allele
<222> 345
<223> 99-7212-346 : polymorphic base C or T

<220>
<221> misc_binding
<222> 333..357
<223> 99-7212-346.probe

<220>
<221> primer_bind
<222> 326..344
<223> 99-7212-346.mis

<220>
<221> primer_bind
<222> 346..364
<223> 99-7212-346.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-7212.pu

<220>
<221> primer_bind
<222> 470..488
<223> 99-7212.rp complement

<400> 19

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gctccttatg taattgaatg aatggtattt ttatcagatg ctttttaaaa gtcagtacac       60
aattccatct atttcacagc aaattctaca gaaatagcag ctagacagca ggaagctgtg      120
gcttactgtt tagtgacttg tgattgtaat taaatgatta gtcttccact ccattccctc      180
caacttgtct tgggtctggg gaggtaggga ggacaaatgc aaaatccata gagtcaagga      240
tatagtgagg agtttacttt gccattgact ctgacaatca atcgtcagtg agacatgctg      300
attgtgatga gaacatgact aaagacaaga ttccttcaag gtagygctct cacgttttca      360
ttcaatgaaa aactattggt gttgtataac ccaatgaatc atttttgtat tttgaatctt      420
taaaaatata tacaagtgct attttgcttg aagtgctgtt tatttataag gttgacaatt      480
aaactgac                                                             488
```

<210> 20
<211> 542
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 226
<223> 99-7193-228 : polymorphic base G or C

<220>
<221> misc_binding
<222> 214..238
<223> 99-7193-228.probe

<220>
<221> primer_bind
<222> 207..225
<223> 99-7193-228.mis

<220>
<221> primer_bind

<222> 227..245
<223> 99-7193-228.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-7193.pu

<220>
<221> primer_bind
<222> 522..542
<223> 99-7193.rp complement

<400> 20
gaggtaaaaa tagcaggcag gagaacagat cttttaggat tgtgaattgt aatgtggaac   60
atgaaaactt catcatcttc tgtgtgctgg ctagtgtcag ttatcctttg ctgtataaaa   120
atcacccccа aaattagtga tttgaaacaa ctgtccccat ttatttactc atgattttgc   180
agttgctcag gacttggtgg ggataccttg actctgcttc tcgcastgtt gactgaqqtc   240
atacttgcag ctacattcag ctggcagctt cattggggct ggaacagcaa agacagcttc   300
cctaacatac ctggcacctc agccaaggtg gctgcaatgg ctggaggctc actgggcctt   360
tcacttctgt gtggtttctc gtgatttcgt agtctatcct gaactccttt tcacggcaac   420
tggaatgcaa aaagatgaaa acagaagcta caatgtctgg gaacagaagt cctagaatgt   480
cacttctact acacctatta ctcactatta gtcaaaataa actcctctcc caatacttct   540
ca   542

<210> 21
<211> 528
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 212
<223> 99-7186-212 : polymorphic base A or G

<220>
<221> misc_binding
<222> 200..224
<223> 99-7186-212.probe

<220>
<221> primer_bind
<222> 193..211
<223> 99-7186-212.mis

<220>
<221> primer_bind
<222> 213..231
<223> 99-7186-212.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-7186.pu

<220>
<221> primer_bind
<222> 510..528
<223> 99-7186.rp complement

<400> 21
gagtgccatg tgtgcataga ttgttgtctg ggttttttcc tttttgttac ttctgcaata   60

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tttagaacag tgactgacac atatcaggca ctcaataatt atttgctgaa tttctcaatg      120
tctcgatttg gcataaggat ttcattttcc catggtatat tttcttccgt ggattgatgg      180
gctagtacta atttgcacgg gtgtcttggt grttcacaat catggtttta atgtcccagt      240
cccctttggc tacaggaggt acttgatcct aggtgactaa ggcagaaata aatagaatgt      300
gtaggactcc tctggtgtaa aaagtcatgg gttccaaaag ttcatttata agtcaattgt      360
ttggacatcc tgaacttatt ttcagaacac gattgggcac agctagttaa ctgcagggag      420
gcctgaggag actggaaggt gccagaacct ggaaccagat ctgcccacta ggacaggacc      480
agccctggaa ggacaggagc aggtgcactg gattctaaag gtgttcag                   528
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<210> 22
<211> 531
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 49
<223> 99-7182-49 : polymorphic base C or T

<220>
<221> misc_binding
<222> 37..61
<223> 99-7182-49.probe

<220>
<221> primer_bind
<222> 30..48
<223> 99-7182-49.mis

<220>
<221> primer_bind
<222> 50..68
<223> 99-7182-49.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-7182.pu

<220>
<221> primer_bind
<222> 511..531
<223> 99-7182.rp complement

<400> 22
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gtgtgtagaa aagaaagatg gctgtcattt gagttgttaa gaacagcayg ctgcaatacc       60
aaaacatcaa gctgtacatc tcaaatatgt atgattttca tatgtgaatc acatctcaat      120
aaagctgtta gaaaaataaa attaccatta agtttaaaaa aaaaagaaa aaaagaaaaa       180
aacaaccaca gtcggggcaa gggccatgtt actagggcca gggatttggc caatgaagca      240
ggaacataga gatcctaggt ccataaggaa aagaagattc aaggaaggcc aggacatggg      300
agggaatgaa caaactccag tcctagaggt ttagcagaga ctagctggct tcttgcagtg      360
aattaataaa tgagaaaaaa atctgagatc acaataaaag atctttactg gtgcaagggc      420
cacttctcac cgctgtttga ctgctttggg tcattcttta gtaccttaag tttttatat      480
tttgtgaaga ttttactatt ttttwatctg caagagagta agttcaatca a             531
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<210> 23
<211> 546
<212> DNA
<213> Homo sapiens

<220>
<221> allele

87

<222> 372
<223> 99-1585-373 : polymorphic base C or T

<220>
<221> misc_binding
<222> 360..384
<223> 99-1585-373.probe

<220>
<221> primer_bind
<222> 353..371
<223> 99-1585-373.mis

<220>
<221> primer_bind
<222> 373..391
<223> 99-1585-373.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-1585.pu

<220>
<221> primer_bind
<222> 527..546
<223> 99-1585.rp complement

<220>
<221> misc_feature
<222> 52..53,55
<223> n=a, g, c or t

<400> 23
cctgcaacat ttttwatgtg tagaattctg tgaatgaatc caacttcggc anntnttttt   60
ttcttttctt tttttttaatc aaggaagtgg agacaagatg tgaaggggtg gcctgcccct   120
ccacacctgt ggatatttct agtcaggtgg gacgagagac tgagaaaata aataaaacac   180
agagacaaag tatagagaaa caacagtggg cccagggaac cggcgctcag cataccaagg   240
acctgcaccg gcaccatctc tgagttccct cagttttat tgattattat cttcgttatt   300
tcagcaaaaa ggaatgtagt aggagagcag ggtgataata aggagaaggt cagcaacgaa   360
catgtgagca ayagaatcta cgtcataatk aagttcaagg gaaggtacta tgactggacg   420
tgcahgtaag ccagatttat gtttctctcc acccaaacat ctcggtggag taaagaataa   480
caaggcagca ttgctgcaaa catgtctcgc ctcccgccat agggcggttt ttctcctatc   540
tcagaa   546

<210> 24
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 278
<223> 99-1587-281 : polymorphic base A or G

<220>
<221> misc_binding
<222> 266..290
<223> 99-1587-281.probe

<220>
<221> primer_bind

<222> 259..277
<223> 99-1587-281.mis

<220>
<221> primer_bind
<222> 279..297
<223> 99-1587-281.mis complement

<220>
<221> primer_bind
<222> 1..21
<223> 99-1587.pu

<220>
<221> primer_bind
<222> 377..396
<223> 99-1587.rp complement

<220>
<221> misc_feature
<222> 48
<223> n=a, g, c or t

<400> 24
taatggtagt tgatgaggtc ctatgtaata tgcatttcct tggttgcnaa tagcaaatta   60
ctacacacac agaaaggaaa gccacactcc ccgacacdwc tacacacagg aggactcaca   120
caggagggag actcaaagaa ggcacgtgac ttttacattg ttagggctta catggtcctg   180
ggatttccca ccagtactca aaagatcaat tgtatgaaca agtcacctat ttttacggca   240
ctaaataatt attattcaac aacatggaaa atatgtgrta gcagacctgg attttcctta   300
agagttattt ttatgtggta ctgccccctg ctggaatata acatctatac acatcctttc   360
tggctgggct gacatcctaa aaccagccca ggacca   396

<210> 25
<211> 447
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 283
<223> 99-13798-284 : polymorphic base A or G

<220>
<221> misc_binding
<222> 271..295
<223> 99-13798-284.probe

<220>
<221> primer_bind
<222> 264..282
<223> 99-13798-284.mis

<220>
<221> primer_bind
<222> 284..302
<223> 99-13798-284.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-13798.pu

<220>
<221> primer_bind
<222> 427..447
<223> 99-13798.rp complement

<220>
<221> misc_feature
<222> 34,416
<223> n=a, g, c or t

<400> 25
gaggaaaagg actttggatg tctggtgtca ctgnctgcac accaggcaca cagcaggtgc   60
tcaataagta tttgatgaat atatcaaatg aatgaggagt gtgacacagt tcaagaagaa   120
aatcaaatga aaaattaggc ttcttagcag cccgaaaaga gctctttatc tagaaattgt   180
caaaccagct gatgcaagtt ttttttggtgt taacaaggca gccgcaagat tgctatggag   240
aggacaccgt gtaccatgga gattaacggc atgagcttta gcrgcagcta accccgtgca   300
gatgtgtgac ttggacaggt tactgagctt gctaagcccc tgtctcactc tccaaacagg   360
gataatgaca cctctctcac aaggtggttg tgaggattaa atgaggtaat cctttnaagc   420
tcccatccta gcacacgtaa gaagcat   447

<210> 26
<211> 506
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 402
<223> 99-1601-402 : polymorphic base A or T

<220>
<221> misc_binding
<222> 390..414
<223> 99-1601-402.probe

<220>
<221> primer_bind
<222> 383..401
<223> 99-1601-402.mis

<220>
<221> primer_bind
<222> 403..421
<223> 99-1601-402.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-1601.pu

<220>
<221> primer_bind
<222> 486..506
<223> 99-1601.rp complement

<400> 26
ttggcttggc agggcaacca gctcaccaga ctctctgcag acccgaagtc attacataca   60
gtatgataac agggaatgga cccgaccagc atttgctgga gatgatatct ggtgtcagcc   120
cgacaggccc ctacctgctt ctcttgatat gcaggaatcc cttcaagctc caacaagatc   180
tgtttaatag actggagagt cctttagttc cttcctctaa gggaaaatca gatcgttctg   240
gtttgcttgg taactcctta cttcatccct gatgggaagt ttatagaatg aggaaccagg   300
gctattacat gaaactataa aactgcctag agcacatact tggtattttt aacattgttg   360

90

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agagggactc acttaattca gccttgcagc tattgcattc cwgtccaaac caacggcagg      420
ttctcaaaac aagcggtgaa agggttcctg ttgcagagct gtctggacat ttaaagaagg      480
gagaggaaat ctcarggggt cggttg                                          506
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<210> 27
<211> 546
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 79
<223> 99-13808-80 : polymorphic base A or T

<220>
<221> misc_binding
<222> 67..91
<223> 99-13808-80.probe

<220>
<221> primer_bind
<222> 60..78
<223> 99-13808-80.mis

<220>
<221> primer_bind
<222> 80..98
<223> 99-13808-80.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-13808.pu

<220>
<221> primer_bind
<222> 526..546
<223> 99-13808.rp complement

<220>
<221> allele
<222> 266
<223> 99-13808-268 : polymorphic base A or C

<220>
<221> misc_binding
<222> 254..278
<223> 99-13808-268.probe

<220>
<221> primer_bind
<222> 247..265
<223> 99-13808-268.mis

<220>
<221> primer_bind
<222> 267..285
<223> 99-13808-268.mis complement

<220>
<221> allele
<222> 419

<223> 99-13808-425 : polymorphic base G or C

<220>
<221> misc_binding
<222> 407..431
<223> 99-13808-425.probe

<220>
<221> primer_bind
<222> 400..418
<223> 99-13808-425.mis

<220>
<221> primer_bind
<222> 420..438
<223> 99-13808-425.mis complement

<220>
<221> allele
<222> 453
<223> 99-13808-455 : polymorphic base A or G

<220>
<221> misc_binding
<222> 441..465
<223> 99-13808-455.probe

<220>
<221> primer_bind
<222> 434..452
<223> 99-13808-455.mis

<220>
<221> primer_bind
<222> 454..472
<223> 99-13808-455.mis complement

<400> 27
gttgtgcctt aaagaatttg ctcatccaca gagtgccaac tgcattagaa agaaaacaac   60
tctcctttct aactcaccwg cattgatttt ctgttgttgg catgtagaag agtatttcaa   120
agaatgaatg aaagctataa tatttattag aagtaaaaaa gttctaaaga tatgctacct   180
tactgggatg cttagagacc atttgcaaac cctgtttatg atctagaaat cctgttttttc   240
atttttttatt tgtaaaactc tataamtctc aaaaaatttt aggtggatta tcatgtacct   300
aagggtaaaa tatagttgaa attattctta cctgattttt catatctgaa tttcgtgggc   360
agttcaaagt aattgtatca cattcttcag ctaggaaaaa aaaaagaaa gaaagaaasa   420
aacaaagtgt gattttaaaa agcacacact ccrtggtgta agacctaaaa ttaaggttca   480
gtgtcacatg ctgccttggc atctggtaaa atcagaagag ctggactaca aatycctctc   540
caaact   546

<210> 28
<211> 476
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 212
<223> 99-13810-214 : polymorphic base C or T

<220>
<221> misc_binding
<222> 200..224

92

<223> 99-13810-214.probe

<220>
<221> primer_bind
<222> 193..211
<223> 99-13810-214.mis

<220>
<221> primer_bind
<222> 213..231
<223> 99-13810-214.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-13810.pu

<220>
<221> primer_bind
<222> 458..476
<223> 99-13810.rp complement

<220>
<221> allele
<222> 168
<223> 99-13810-170 : polymorphic base A or T

<220>
<221> misc_binding
<222> 156..180
<223> 99-13810-170.probe

<220>
<221> primer_bind
<222> 149..167
<223> 99-13810-170.mis

<220>
<221> primer_bind
<222> 169..187
<223> 99-13810-170.mis complement

<400> 28
gcattcccag attgtaacat agttttaagt aaacatccac tgaaagtctg catggaagaa   60
cacagaagcc agagcaagtt cagggctcct agaaagacga tgctggagct agccctagag   120
aatggctgag aattggatga actcagaaga agcagcaaag tagttgcwgg tggcaggcat   180
ggcaggagaa gggatcaggt ggctggaaga gyggagggta tagaactgaa acagagagtc   240
tgttggaggt ggacagagga aggcgggatt agatgagaaa tgacggaccc agtttctaag   300
aaagaccaag aaagataagc aaagggattt aggtgggatg cccttctagg ttctcgggaa   360
acttgctacc tgccttgcac tgactttgca tgaggaaga tggtcaacac agtcttgcaa   420
gaagtcagac aagcaggcaa tgacaattct ctgagatggc aaatagggat tgggct   476

<210> 29
<211> 454
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 127
<223> 99-13790-129 : polymorphic base C or T

<220>
<221> misc_binding
<222> 115..139
<223> 99-13790-129.probe

<220>
<221> primer_bind
<222> 108..126
<223> 99-13790-129.mis

<220>
<221> primer_bind
<222> 128..146
<223> 99-13790-129.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-13790.pu

<220>
<221> primer_bind
<222> 434..454
<223> 99-13790.rp complement

<400> 29
gtcattttac taagccttc agacagtaga gagtgggatt atacttgtcc caacagctca   60
ccctcctaaa ggtcaaacct aaaccatttt ggttctcttg ttcaagttca ggttgccagt   120
gaaaagyaaa ggaacttgaa attcatgtta aacatttaac atctttccat atgaattgct   180
aggaagcaac ttccattcca aagttgtgtt aacttcacag ttttcccacc tgtggtgaag   240
atggtacaaa atagcttaaa aactgatttt gttccatcag attctaatct ttagtcacag   300
aattcaaggc catactctaa actttaaggt tggcagaaat atattataac agaaatttta   360
gcaccatgta aatgtttaaa gttatttagc cttaaataca gaaccattta actcagggtt   420
gaaaagtcag gatgaagtga gggwttgatt gatt   454

<210> 30
<211> 444
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 153
<223> 99-13809-153 : polymorphic base A or G

<220>
<221> misc_binding
<222> 141..165
<223> 99-13809-153.probe

<220>
<221> primer_bind
<222> 134..152
<223> 99-13809-153.mis

<220>
<221> primer_bind
<222> 154..172
<223> 99-13809-153.mis complement

<220>
<221> primer_bind

<222> 1..21
<223> 99-13809.pu

<220>
<221> primer_bind
<222> 424..444
<223> 99-13809.rp complement

<400> 30
caactgagtg aagagcaatg ggaatttgta gactttacag atgacatcac ccccatcata   60
cacgatgaag ctcagcagac agttgctgct ttccatccct taaccaggat atccctgata   120
aaggaaggac ccaagattag caaaactggc caracttcag gcagtcatct tattgctgga   180
tgtcctggcc aacaaatcgc cccatctgca cagtttttat aaatttttgg accattgcct   240
aagagttgca ccctttgtgg taaagaactc tcagaatctc ttgcctcaaa tacacccaaa   300
ctataaataa agaaacagat gtctctatgt acagcaaggc caccatacaa ggcttcagca   360
gaacatttcc agtctccttt ggagtcccac ttattactga cagtgagcaa gacactcatt   420
tctcttctaa gaacatacaa cgcc   444

<210> 31
<211> 693
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 162
<223> 99-1597-162 : polymorphic base A or G

<220>
<221> misc_binding
<222> 150..174
<223> 99-1597-162.probe

<220>
<221> primer_bind
<222> 143..161
<223> 99-1597-162.mis

<220>
<221> primer_bind
<222> 163..181
<223> 99-1597-162.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-1597.pu

<220>
<221> primer_bind
<222> 675..693
<223> 99-1597.rp complement

<220>
<221> misc_feature
<222> 582..615
<223> n=a, g, c or t

<400> 31
tttaagatgc caagttgtca aactgggcag ctaggcccca ggctctttct aaattgtcaa   60
gactagcaaa gccgagtcat cccccctgctc tagttctgga tgacaccaag cctaggaaat   120
aaagcacaat agatggggcc ctggtctctg aatgacagag trtgcatggg ggctaggagg   180

95

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aaggaggaat ccagctctct aaaaggaagg tgcaggcggt gtgtgagggg tcaaagacaa      240
aggggcgtgt cccactgaag atacaaactc taggccgggc gcggtggctc atgcctgtaa      300
tcccagtact ttgggatgcc aaggcgggca gatcacaagg tcaggagatc gagaccatct      360
tggctaaggg ggtgaaaccc tgtctctact aaaaaaacta caaaaagtta gccaggtgtg      420
gtagcatacg cctgtagtcc cagctactca ggaggctgag gcaggagaat tgcttgaacc      480
cgggagatgg aggttgcagt gagccaagat cacgccactg cactccagcc tgggcaacag      540
agcgagactc tgtctcaaaa aggaaaagaa aaagaaaaag annnnnnnnn nnnnnnnnnn      600
nnnnnnnnnn nnnnnaatag atttctgttt ccttgatgag gaaacaagat aaaactagtc      660
actatgtatt gggtggctac tttagcatca atc                                  693


<210> 32
<211> 26
<212> DNA
<213> Artificial Sequence


<220>
<223> oligonucleotide BAP283Ra6283


<400> 32
ggcggatgac tctctttgga aaccac                                           26


<210> 33
<211> 25
<212> DNA
<213> Artificial Sequence


<220>
<223> oligonucleotide BAP283Ra6324n


<400> 33
tgctaaagac gagagactcc tcgcc                                            25


<210> 34
<211> 29
<212> DNA
<213> Artificial Sequence


<220>
<223> oligonucleotide BAP28-exALF7311


<400> 34
cccccctatga tctgattcac caggcttac                                       29


<210> 35
<211> 26
<212> DNA
<213> Artificial Sequence


<220>
<223> oligonucleotide BAP28-exALF7319n


<400> 35
gatctgattc accaggctta cctccg                                           26


<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence


<220>
<223> oligonucleotide PCTAexALF12
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<400> 36
cccacctgaa aagactggat ttgggac   27

<210> 37
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTAexALF13n

<400> 37
ccacctgaaa agactggatt tgggaca   27

<210> 38
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTAexALR60

<400> 38
ctccgaagtt ctacaggatc atgtccc   27

<210> 39
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTAexALR12n

<400> 39
cccaaatcca gtcttttcag gtgggag   27

<210> 40
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTAexBLF33

<400> 40
gaaaaccctg gcgttgaccc cgtgg   25

<210> 41
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTAexBLF120n

<400> 41
caccctggtc ctgaaaagtc cagcc   25

<210> 42
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTAexBLR140

<400> 42
taggagggag ggagattcgg ggctg   25

<210> 43
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTAexBLR40n

<400> 43
tccacggggt caacgccagg gttttc   26

<210> 44
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTA5Ra220n

<400> 44
gggaatggtg ccaacatacg ggattac   27

<210> 45
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTA5Ra230

<400> 45
gctgatcggg aatggtgcca acatac   26

<210> 46
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTA_5Ra400

<400> 46
tcacctacac ctcacccact tcctc   25

<210> 47
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTA_5Ran_400

<400> 47
cctacacctc acccacttcc tcccc   25

<210> 48
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTA_5Ra_394

<400> 48
cctccccacc actggttcat tttgaag   27

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTA exD5Ra

<400> 49
tccccaggaa gtgtcatgga cggtg   25

<210> 50
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTA_exD5Ran

<400> 50
ggaagtgtca tggacggtgt cttctac   27

<210> 51
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTA_exC5Ra

<400> 51
gctttcatcg cccagctcca gcaattatc   29

<210> 52
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTA_exC5Ran

<400> 52
tcgcccagct ccagcaatta tcgac   25

<210> 53
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide PCTAex9terLR330

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<400> 53
acatggggag ctgtgacagt tctgg                                              25


<210> 54
<211> 29
<212> DNA
<213> Artificial Sequence


<220>
<223> oligonucleotide PCTAex9terLR325n

<400> 54
ggggagctgt gacagttctg gaacataag                                         29


<210> 55
<211> 27
<212> DNA
<213> Artificial Sequence


<220>
<223> oligonucleotide PCTAexCLF120

<400> 55
cttcaaaatg aaccagtggt ggggagg                                           27


<210> 56
<211> 25
<212> DNA
<213> Artificial Sequence


<220>
<223> oligonucleotide PCTAexCLF130n

<400> 56
accagtggtg gggaggaagt gggtg                                             25


<210> 57
<211> 20
<212> DNA
<213> Artificial Sequence


<220>
<223> oligonucleotide BAP28polyTcourt

<400> 57
tttttttttt tttttgtata                                                   20


<210> 58
<211> 25
<212> DNA
<213> Artificial Sequence


<220>
<223> oligonucleotide BAP281LF12.1

<400> 58
ccatgtggga agcgctgtga agagt                                             25


<210> 59
<211> 26
<212> DNA
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<213> Artificial Sequence

<220>
<223> oligonucleotide BAP28LR6726.1

<400> 59
cagctctata cgataggcag gagagg   26

<210> 60
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide BAP28LF26SalI

<400> 60
cctgtgtcga ccgctgtgaa gagttgttgc cttccaag   38

<210> 61
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide BAP28LR6717SalI

<400> 61
actccgtcga ccgataggca ggagaggctt atgtgg   36

<210> 62
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> sequencing oligonucleotide PrimerPU

<400> 62
tgtaaaacga cggccagt   18

<210> 63
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> sequencing oligonucleotide PrimerRP

<400> 63
caggaaacag ctatgacc   18